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Title: US-09-580-015-42_COPY_1_12
Perfect score: 12
Sequence: 1 DAEFRHDSGYEV 12

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Searched: 231628 seqs, 24425594 residues

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SUMMARIES

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354 4 33.3 7 1 US-08-136-743B-35 Sequence 35, Appli
355 4 33.3 7 1 US-08-136-743B-56 Sequence 56, Appli
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359 4 33.3 7 4 US-09-173-941-82 Sequence 82, Appli
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363 4 33.3 9 3 US-08-802-981-221 Sequence 221, App
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365 4 33.3 9 6 517197-3 Patent No. 517197
366 4 33.3 10 2 US-08-025-321C-1 Sequence 1, Appli
367 4 33.3 10 2 US-08-764-640-119 Sequence 119, App
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370 4 33.3 10 4 US-08-480-332-9 Sequence 9, Appli
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376 4 33.3 21 3 US-08-802-981-113 Sequence 112, App
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386 4 33.3 26 1 US-08-475-989-27 Sequence 89, Appli
387 4 33.3 26 2 US-08-482-142-89 Sequence 89, Appli
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389 4 33.3 26 2 US-08-475-985-27 Sequence 27, Appli
390 4 33.3 26 3 US-08-256-839-27 Sequence 27, Appli
391 4 33.3 26 4 US-08-484-296-89 Sequence 89, Appli
392 4 33.3 27 3 US-09-045-632-92 Sequence 92, Appli

393	4	33.3	28	4	US-09-227-357-634	Sequence 634, App	456	4	33.3	83	4	US-09-103-434-10	Sequence 10, Appl
394	4	33.3	29	2	US-08-482-142-101	Sequence 101, App	467	4	33.3	83	4	US-09-687-594-10	Sequence 10, Appl
395	4	33.3	29	2	US-08-478-572-101	Sequence 101, App	468	4	33.3	84	4	US-09-045-632-4	Sequence 4, Appl
396	4	33.3	29	4	US-08-484-296-101	Sequence 101, App	469	4	33.3	91	2	US-08-997-080-143	Sequence 143, App
397	4	33.3	30	1	US-08-352-179-20	Sequence 20, Appl	470	4	33.3	91	2	US-08-997-362-143	Sequence 143, App
398	4	33.3	30	2	US-08-659-984A-17	Sequence 17, Appl	471	4	33.3	91	4	US-09-095-855-143	Sequence 143, App
399	4	33.3	30	2	US-08-660-531-17	Sequence 17, Appl	472	4	33.3	91	4	US-09-324-542-143	Sequence 6, Appl
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401	4	33.3	34	3	US-08-974-549A-256	Sequence 256, App	474	4	33.3	103	4	US-09-374-135-5	Sequence 5, Appl
402	4	33.3	34	4	US-08-854-050-138	Sequence 138, App	475	4	33.3	106	4	US-08-858-207A-326	Sequence 326, App
403	4	33.3	34	4	US-09-430-323-138	Sequence 138, App	476	4	33.3	109	3	US-09-053-197A-16	Sequence 16, Appl
404	4	33.3	37	1	US-08-352-179-19	Sequence 19, Appl	477	4	33.3	109	4	US-09-085-761A-16	Sequence 16, Appl
405	4	33.3	38	1	US-08-176-500-67	Sequence 67, Appl	478	4	33.3	111	1	US-08-369-796-15	Sequence 15, Appl
406	4	33.3	38	1	US-08-176-500-68	Sequence 68, Appl	479	4	33.3	111	2	US-08-852-091-15	Sequence 15, Appl
407	4	33.3	38	1	US-08-471-052A-67	Sequence 67, Appl	480	4	33.3	111	5	PCT-US95-17025-15	Sequence 15, Appl
408	4	33.3	38	1	US-08-471-052A-68	Sequence 68, Appl	481	4	33.3	118	2	US-08-443-639-13	Sequence 13, Appl
409	4	33.3	38	1	US-08-189-331-67	Sequence 67, Appl	482	4	33.3	118	3	US-08-577-483-13	Sequence 13, Appl
410	4	33.3	38	1	US-08-189-331-68	Sequence 68, Appl	483	4	33.3	118	3	US-08-936-165A-464	Sequence 464, App
411	4	33.3	38	1	US-08-471-939-68	Sequence 68, Appl	484	4	33.3	120	4	US-08-679-006-34	Sequence 34, Appl
412	4	33.3	38	2	US-08-471-939-68	Sequence 68, Appl	485	4	33.3	123	1	US-08-356-272-3	Sequence 3, Appl
413	4	33.3	38	2	US-08-471-800-67	Sequence 67, Appl	486	4	33.3	123	4	US-08-858-207A-320	Sequence 320, App
414	4	33.3	38	2	US-08-471-068-67	Sequence 67, Appl	487	4	33.3	124	1	US-08-462-949-26	Sequence 26, Appl
415	4	33.3	38	2	US-08-471-068-68	Sequence 68, Appl	488	4	33.3	124	1	US-08-023-764B-26	Sequence 26, Appl
416	4	33.3	38	2	US-08-471-068-68	Sequence 68, Appl	489	4	33.3	127	2	US-08-637-759B-198	Sequence 198, App
417	4	33.3	39	1	US-08-038-343A-1	Sequence 1, Appl	490	4	33.3	127	3	US-08-871-355A-198	Sequence 198, App
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419	4	33.3	40	3	US-09-035-619-23	Sequence 23, Appl	492	4	33.3	131	1	US-07-893-929A-1	Sequence 1, Appl
420	4	33.3	40	3	US-09-035-619-24	Sequence 24, Appl	493	4	33.3	131	5	PCT-US92-10344-1	Sequence 8, Appl
421	4	33.3	40	3	US-09-035-619-25	Sequence 25, Appl	494	4	33.3	133	1	US-08-268-348A-8	Sequence 8, Appl
422	4	33.3	40	4	US-09-514-006-22	Sequence 22, Appl	495	4	33.3	137	1	US-07-745-206A-32	Sequence 32, Appl
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425	4	33.3	40	4	US-09-514-006-25	Sequence 25, Appl	498	4	33.3	138	2	US-08-824-405-10	Sequence 10, Appl
426	4	33.3	41	1	US-08-232-018-5	Sequence 5, Appl	499	4	33.3	143	4	US-08-858-207A-441	Sequence 41, App
427	4	33.3	41	1	US-08-504-047-5	Sequence 5, Appl	500	4	33.3	148	4	US-08-818-112-64	Sequence 64, Appl
428	4	33.3	41	2	US-09-087-855-5	Sequence 5, Appl	501	4	33.3	148	4	US-08-818-111-65	Sequence 65, Appl
429	4	33.3	41	3	US-08-491-954-38	Sequence 38, Appl	502	4	33.3	157	3	US-09-056-556-64	Sequence 64, Appl
430	4	33.3	41	4	US-09-257-218-9	Sequence 9, Appl	503	4	33.3	157	3	US-08-851-843A-83	Sequence 83, Appl
431	4	33.3	41	4	US-09-257-218-11	Sequence 11, Appl	504	4	33.3	157	4	US-08-974-549A-226	Sequence 226, App
432	4	33.3	41	4	US-09-311-760-9	Sequence 9, Appl	505	4	33.3	157	4	US-08-854-050-83	Sequence 83, Appl
433	4	33.3	41	4	US-09-311-760-11	Sequence 11, Appl	506	4	33.3	159	4	US-09-095-855-136	Sequence 136, App
434	4	33.3	41	6	5177197-35	Patent No. 5177197	507	4	33.3	161	3	US-09-045-631-14	Sequence 14, Appl
435	4	33.3	42	1	US-08-271-162-5	Sequence 5, Appl	508	4	33.3	161	4	US-09-158-843A-14	Sequence 14, Appl
436	4	33.3	42	1	US-08-268-348A-2	Sequence 2, Appl	509	4	33.3	163	2	US-08-858-207A-284	Sequence 284, App
437	4	33.3	42	4	US-08-974-549A-96	Sequence 96, Appl	510	4	33.3	163	2	US-08-704-931-6	Sequence 6, Appl
438	4	33.3	42	5	PCT-US95-08302-5	Sequence 5, Appl	511	4	33.3	163	2	US-08-245-511-23	Sequence 23, Appl
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441	4	33.3	43	6	5187153-12	Patent No. 5187153	514	4	33.3	166	2	US-09-237-507-4	Sequence 4, Appl
442	4	33.3	45	1	US-08-366-690-3	Sequence 3, Appl	515	4	33.3	168	2	US-09-087-465-28	Sequence 28, Appl
443	4	33.3	45	4	US-08-936-165A-274	Sequence 274, App	516	4	33.3	173	4	US-09-232-191-35	Sequence 35, Appl
444	4	33.3	47	4	US-08-974-549A-42	Sequence 42, Appl	517	4	33.3	173	4	US-09-232-200-87	Sequence 87, Appl
445	4	33.3	55	1	US-07-676-647-3	Sequence 3, Appl	518	4	33.3	173	4	US-09-232-197-87	Sequence 87, Appl
446	4	33.3	55	1	US-08-449-329-3	Sequence 3, Appl	519	4	33.3	173	4	US-09-232-201-87	Sequence 87, Appl
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448	4	33.3	55	2	US-08-585-258-3	Sequence 3, Appl	521	4	33.3	175	3	US-09-158-843A-10	Sequence 10, Appl
449	4	33.3	55	4	US-09-211-590-3	Sequence 3, Appl	522	4	33.3	175	4	US-08-975-762-29	Sequence 29, Appl
450	4	33.3	55	5	PCT-US91-03896-3	Sequence 3, Appl	523	4	33.3	175	4	US-08-821-324-29	Sequence 29, Appl
451	4	33.3	61	3	US-08-605-150A-16	Sequence 16, Appl	524	4	33.3	175	4	US-09-235-028-29	Sequence 29, Appl
452	4	33.3	66	1	US-07-626-618A-16	Sequence 16, Appl	525	4	33.3	175	4	US-09-106-582-29	Sequence 29, Appl
453	4	33.3	66	1	US-07-928-611-16	Sequence 16, Appl	526	4	33.3	177	1	US-08-850-118-4	Sequence 4, Appl
454	4	33.3	66	2	US-08-333-977-16	Sequence 16, Appl	527	4	33.3	177	2	US-09-008-253-4	Sequence 4, Appl
455	4	33.3	66	2	US-08-487-811A-16	Sequence 16, Appl	528	4	33.3	177	3	US-09-093-335-4	Sequence 4, Appl
456	4	33.3	66	4	US-09-060-694-16	Sequence 16, Appl	529	4	33.3	188	1	US-08-233-389C-3	Sequence 3, Appl
457	4	33.3	66	5	PCT-US93-07370-16	Sequence 16, Appl	530	4	33.3	188	2	US-08-801-863-3	Sequence 3, Appl
458	4	33.3	69	4	US-08-936-165A-458	Sequence 458, App	531	4	33.3	188	2	US-08-486-596A-3	Sequence 3, Appl
459	4	33.3	70	4	US-08-280-443-21	Sequence 21, Appl	532	4	33.3	188	2	US-09-004-713-3	Sequence 3, Appl
460	4	33.3	74	1	US-08-457-459-21	Sequence 21, Appl	533	4	33.3	192	4	US-09-500-569-8	Sequence 8, Appl
461	4	33.3	74	1	US-08-555-678-21	Sequence 21, Appl	534	4	33.3	192	4	US-08-953-139-2	Sequence 2, Appl
462	4	33.3	74	5	PCT-US95-02275-21	Sequence 21, Appl	535	4	33.3	193	1	US-08-953-139-4	Sequence 4, Appl
463	4	33.3	81	4	US-08-858-207A-537	Sequence 537, App	536	4	33.3	193	1	US-08-260-202A-19	Sequence 19, Appl
464	4	33.3	83	2	US-08-726-136-10	Sequence 10, Appl	537	4	33.3	193	1	US-08-017-114-19	Sequence 19, Appl
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540	4	33.3	193	5	PCT-US94-02034-19	Sequence 19, Appl	613	4	33.3	268	2	US-08-687-559-25	Sequence 25, Appl
541	4	33.3	197	4	US-08-996-408-2	Sequence 2, Appl	614	4	33.3	270	4	US-09-693-147-4	Sequence 4, Appl
542	4	33.3	197	4	US-09-310-847-2	Sequence 2, Appl	615	4	33.3	271	3	US-09-045-631-4	Sequence 4, Appl
543	4	33.3	197	4	US-09-310-845-2	Sequence 2, Appl	616	4	33.3	271	3	US-09-045-631-6	Sequence 4, Appl
544	4	33.3	197	4	US-09-548-023-2	Sequence 2, Appl	617	4	33.3	271	3	US-09-158-843A-4	Sequence 4, Appl
545	4	33.3	198	3	US-09-045-632-11	Sequence 11, Appl	618	4	33.3	271	4	US-09-158-843A-6	Sequence 6, Appl
546	4	33.3	199	2	US-08-211-312-6	Sequence 6, Appl	619	4	33.3	274	4	US-08-867-030B-15	Sequence 15, Appl
547	4	33.3	199	3	US-08-472-285-6	Sequence 6, Appl	620	4	33.3	274	5	PCT-US95-06119-15	Sequence 15, Appl
548	4	33.3	199	3	US-08-472-929-6	Sequence 6, Appl	621	4	33.3	277	1	US-07-800-364B-14	Sequence 14, Appl
549	4	33.3	202	2	US-08-286-819A-6	Sequence 6, Appl	622	4	33.3	281	2	US-07-989-847-12	Sequence 12, Appl
550	4	33.3	202	3	US-08-980-357-6	Sequence 6, Appl	623	4	33.3	281	2	US-08-469-411-12	Sequence 12, Appl
551	4	33.3	202	4	US-09-018-635-49	Sequence 49, Appl	624	4	33.3	281	3	US-08-911-853-37	Sequence 37, Appl
552	4	33.3	204	2	US-08-531-525-32	Sequence 32, Appl	625	4	33.3	282	3	US-09-479-409-37	Sequence 37, Appl
553	4	33.3	204	2	US-08-718-270A-32	Sequence 32, Appl	626	4	33.3	282	4	US-09-377-557-6	Sequence 37, Appl
554	4	33.3	206	1	US-08-097-827-7	Sequence 7, Appl	627	4	33.3	282	4	US-08-437-607A-2	Sequence 7, Appl
555	4	33.3	206	1	US-08-494-574-7	Sequence 7, Appl	628	4	33.3	283	4	US-09-105-697-8	Sequence 8, Appl
556	4	33.3	212	2	US-08-761-248B-2	Sequence 2, Appl	629	4	33.3	284	2	US-09-105-697-5	Sequence 5, Appl
557	4	33.3	212	2	US-08-807-300-3	Sequence 3, Appl	630	4	33.3	284	3	US-09-045-632-12	Sequence 12, Appl
558	4	33.3	214	3	US-08-807-300-3	Sequence 3, Appl	631	4	33.3	284	3	US-09-053-197A-2	Sequence 2, Appl
559	4	33.3	215	6	5455030-3	Patent No. 5455030	632	4	33.3	284	3	US-09-085-761A-2	Sequence 2, Appl
560	4	33.3	217	1	US-08-232-018-2	Sequence 2, Appl	633	4	33.3	287	2	US-09-105-697-7	Sequence 7, Appl
561	4	33.3	217	1	US-08-232-018-3	Sequence 3, Appl	634	4	33.3	287	4	US-09-105-697-5	Sequence 5, Appl
562	4	33.3	217	1	US-08-504-047-2	Sequence 2, Appl	635	4	33.3	288	4	US-09-105-697-6	Sequence 6, Appl
563	4	33.3	217	1	US-08-504-047-3	Sequence 3, Appl	636	4	33.3	288	4	US-09-082-614A-52	Sequence 52, Appl
564	4	33.3	217	2	US-08-726-136-2	Sequence 2, Appl	637	4	33.3	289	4	US-08-459-499-16	Sequence 16, Appl
565	4	33.3	217	2	US-08-640-808-2	Sequence 2, Appl	638	4	33.3	291	4	US-08-158-735A-17	Sequence 17, Appl
566	4	33.3	217	2	US-09-087-855-2	Sequence 2, Appl	639	4	33.3	291	4	US-08-680-726A-80	Sequence 80, Appl
567	4	33.3	217	2	US-09-087-855-3	Sequence 3, Appl	640	4	33.3	291	4	US-09-092-409-80	Sequence 80, Appl
568	4	33.3	217	4	US-09-103-434-2	Sequence 2, Appl	641	4	33.3	293	2	US-08-807-050-1	Sequence 25, Appl
569	4	33.3	217	4	US-09-687-594-2	Sequence 2, Appl	642	4	33.3	293	2	US-08-484-956-88	Sequence 1, Appl
570	4	33.3	218	1	US-08-417-822A-2	Sequence 2, Appl	643	4	33.3	293	3	US-08-757-653-88	Sequence 88, Appl
571	4	33.3	218	2	US-08-336-031-4	Sequence 4, Appl	644	4	33.3	300	4	US-09-166-412-4	Sequence 4, Appl
572	4	33.3	218	2	US-08-531-525-19	Sequence 19, Appl	645	4	33.3	305	1	US-08-592-411-15	Sequence 15, Appl
573	4	33.3	218	2	US-08-718-270A-19	Sequence 19, Appl	646	4	33.3	305	1	US-09-387-574-4	Sequence 4, Appl
574	4	33.3	218	5	PCT-US95-06725-4	Sequence 4, Appl	647	4	33.3	307	3	US-09-668-096-4	Sequence 4, Appl
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576	4	33.3	220	4	US-09-052-089A-4	Sequence 4, Appl	649	4	33.3	310	2	US-08-118-270-28	Sequence 28, Appl
577	4	33.3	223	4	US-08-961-083-162	Sequence 162, App	650	4	33.3	310	2	US-08-484-956-88	Sequence 88, Appl
578	4	33.3	223	4	US-09-377-557-16	Sequence 16, Appl	651	4	33.3	310	4	US-08-757-653-88	Sequence 88, Appl
579	4	33.3	223	4	US-09-516-914-13	Sequence 13, Appl	652	4	33.3	310	4	US-09-372-934-4	Sequence 4, Appl
580	4	33.3	225	4	US-08-821-994-49	Sequence 49, Appl	653	4	33.3	313	1	US-08-592-411-15	Sequence 15, Appl
581	4	33.3	228	2	US-08-766-982-11	Sequence 11, Appl	654	4	33.3	313	4	US-09-387-574-4	Sequence 4, Appl
582	4	33.3	228	3	US-09-045-631-8	Sequence 8, Appl	655	4	33.3	313	4	US-09-668-096-4	Sequence 4, Appl
583	4	33.3	228	4	US-09-158-843A-8	Sequence 8, Appl	656	4	33.3	314	1	US-08-592-411-17	Sequence 17, Appl
584	4	33.3	228	4	US-08-944-483-55	Sequence 55, Appl	657	4	33.3	315	1	US-08-118-270-28	Sequence 28, Appl
585	4	33.3	228	4	US-09-296-219-11	Sequence 11, Appl	658	4	33.3	315	2	US-08-484-956-88	Sequence 88, Appl
586	4	33.3	230	4	US-08-821-994-50	Sequence 50, Appl	659	4	33.3	315	2	US-08-757-653-91	Sequence 91, Appl
587	4	33.3	233	3	US-08-851-843A-64	Sequence 64, Appl	660	4	33.3	315	5	PCT-US93-08528-28	Sequence 28, Appl
588	4	33.3	233	4	US-08-974-549A-15	Sequence 15, Appl	661	4	33.3	316	4	US-09-241-750-2	Sequence 2, Appl
589	4	33.3	233	4	US-08-854-050-64	Sequence 64, Appl	662	4	33.3	317	4	US-08-913-159-14	Sequence 14, Appl
590	4	33.3	233	4	US-09-430-323-64	Sequence 64, Appl	663	4	33.3	320	2	US-08-757-653-163	Sequence 163, App
591	4	33.3	234	1	US-08-850-118-2	Sequence 2, Appl	664	4	33.3	320	2	US-08-823-516-61	Sequence 61, Appl
592	4	33.3	234	2	US-09-008-253-2	Sequence 2, Appl	665	4	33.3	320	3	US-08-759-038-102	Sequence 102, App
593	4	33.3	234	3	US-09-093-335-2	Sequence 2, Appl	666	4	33.3	320	3	US-08-852-730-9	Sequence 9, Appl
594	4	33.3	234	4	US-08-771-321-2	Sequence 2, Appl	667	4	33.3	320	3	US-08-758-314-102	Sequence 102, App
595	4	33.3	236	1	US-08-684-862-5	Sequence 5, Appl	668	4	33.3	321	1	US-07-945-288-6	Sequence 6, Appl
596	4	33.3	241	2	US-08-286-819A-42	Sequence 42, Appl	669	4	33.3	321	1	US-08-462-831-6	Sequence 6, Appl
597	4	33.3	241	3	US-08-980-357-42	Sequence 42, Appl	670	4	33.3	321	1	US-08-461-809-6	Sequence 6, Appl
598	4	33.3	244	4	US-08-821-994-80	Sequence 80, Appl	671	4	33.3	321	1	US-08-461-441-6	Sequence 6, Appl
599	4	33.3	245	4	US-09-171-461-15	Sequence 15, Appl	672	4	33.3	321	2	US-08-482-142-6	Sequence 6, Appl
600	4	33.3	246	2	US-08-704-931-2	Sequence 2, Appl	673	4	33.3	321	2	US-08-478-572-6	Sequence 6, Appl
601	4	33.3	251	2	US-08-834-655-7	Sequence 7, Appl	674	4	33.3	321	4	US-08-484-296-6	Sequence 6, Appl
602	4	33.3	252	2	US-08-834-655-7	Sequence 7, Appl	675	4	33.3	321	5	PCT-US93-08518-6	Sequence 6, Appl
603	4	33.3	252	3	US-08-834-655-7	Sequence 7, Appl	676	4	33.3	322	2	US-08-484-296-6	Sequence 6, Appl
604	4	33.3	252	4	US-09-363-574-7	Sequence 7, Appl	677	4	33.3	322	2	US-08-484-296-6	Sequence 6, Appl
605	4	33.3	260	2	US-09-172-977-1	Sequence 1, Appl	678	4	33.3	322	2	US-08-484-296-6	Sequence 6, Appl
606	4	33.3	263	2	US-08-809-267-4	Sequence 4, Appl	679	4	33.3	323	6	517840-6	Patent No. 517840
607	4	33.3	263	2	US-08-149-097D-28	Sequence 28, Appl	680	4	33.3	323	6	517840-6	Patent No. 517840
608	4	33.3	263	5	PCT-US95-13662A-4	Sequence 4, Appl	681	4	33.3	325	3	US-08-303-861-12	Sequence 12, Appl
609	4	33.3	265	2	US-08-937-931-6	Sequence 6, Appl	682	4	33.3	325	4	US-08-975-762-8	Sequence 8, Appl
610	4	33.3	265	4	US-09-285-502-6	Sequence 6, Appl	683	4	33.3	325	4	US-08-821-324-8	Sequence 8, Appl
611	4	33.3	265	4	US-09-709-126-6	Sequence 6, Appl	684	4	33.3	325	4	US-09-295-028-8	Sequence 8, Appl
												US-09-106-582-8	Sequence 8, Appl

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696	4	33.3	342	5	PCT-US94-08326-14	Sequence 14, Appli	769	4	33.3	399	1	US-08-406-672-23	Sequence 23, Appli
697	4	33.3	344	6	5171840-7	Patent No. 5171840	770	4	33.3	399	1	US-08-643-563A-23	Sequence 23, Appli
698	4	33.3	344	6	5480796-7	Patent No. 5480796	771	4	33.3	399	1	US-08-447-570-27	Sequence 27, Appli
699	4	33.3	346	4	US-08-915-498B-31	Sequence 31, Appli	772	4	33.3	399	1	US-08-643-763A-23	Sequence 23, Appli
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740	4	33.3	387	1	US-08-449-651-1	Sequence 1, Appli	813	4	33.3	402	1	US-08-147-023-29	Sequence 29, Appli
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742	4	33.3	387	2	US-08-486-839-6	Sequence 6, Appli	815	4	33.3	402	1	US-08-278-729A-21	Sequence 21, Appli
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834	4	33.3	402	3	US-08-445-467-21	Sequence 21, Appl	907	4	33.3	430	2	US-08-449-700-25	Sequence 25, Appl
835	4	33.3	402	3	US-08-460-515A-21	Sequence 8, Appl	908	4	33.3	430	2	US-08-449-699A-25	Sequence 25, Appl
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841	4	33.3	402	5	PCT-US93-07189-6	Sequence 6, Appl	914	4	33.3	430	3	US-08-480-515A-19	Sequence 19, Appl
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843	4	33.3	402	5	PCT-US93-07231-21	Sequence 21, Appl	916	4	33.3	430	4	US-09-170-936-19	Sequence 19, Appl
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849	4	33.3	408	1	US-08-147-023-15	Sequence 15, Appl	922	4	33.3	430	5	PCT-US93-04392-12	Sequence 12, Appl
850	4	33.3	408	1	US-08-447-570-15	Sequence 15, Appl	923	4	33.3	430	5	PCT-US93-04392-15	Sequence 15, Appl
851	4	33.3	408	2	US-08-449-700-15	Sequence 15, Appl	924	4	33.3	430	5	PCT-US93-05446-9	Sequence 9, Appl
852	4	33.3	408	2	US-08-449-699A-15	Sequence 15, Appl	925	4	33.3	430	5	PCT-US93-07189-4	Sequence 4, Appl
853	4	33.3	409	4	US-09-029-755C-2	Sequence 2, Appl	926	4	33.3	430	5	PCT-US93-07190-19	Sequence 19, Appl
854	4	33.3	410	5	PCT-US91-01861-3	Sequence 3, Appl	927	4	33.3	430	5	PCT-US93-07231-19	Sequence 19, Appl
855	4	33.3	411	2	US-08-336-031-2	Sequence 2, Appl	928	4	33.3	430	5	PCT-US93-08742-19	Sequence 19, Appl
856	4	33.3	411	2	US-08-902-853-7	Sequence 7, Appl	929	4	33.3	430	5	PCT-US93-08808-19	Sequence 19, Appl
857	4	33.3	411	5	PCT-US95-06725-2	Sequence 2, Appl	930	4	33.3	430	5	PCT-US93-08885-19	Sequence 19, Appl
858	4	33.3	412	1	US-08-132-405-3	Sequence 3, Appl	931	4	33.3	430	5	PCT-US93-10520-6	Sequence 6, Appl
859	4	33.3	412	1	US-08-395-939A-3	Sequence 3, Appl	932	4	33.3	431	1	US-07-841-646-2	Sequence 2, Appl
860	4	33.3	412	2	US-08-463-081B-14	Sequence 14, Appl	933	4	33.3	431	1	US-07-901-703-2	Sequence 2, Appl
861	4	33.3	412	2	US-08-461-379A-14	Sequence 14, Appl	934	4	33.3	431	1	US-07-539-756-4	Sequence 4, Appl
862	4	33.3	412	2	US-08-462-390B-14	Sequence 14, Appl	935	4	33.3	431	1	US-08-147-023-2	Sequence 2, Appl
863	4	33.3	412	2	US-08-851-088-12	Sequence 12, Appl	936	4	33.3	431	1	US-08-206-864-2	Sequence 2, Appl
864	4	33.3	412	2	US-08-463-074B-14	Sequence 14, Appl	937	4	33.3	431	1	US-08-278-729A-17	Sequence 17, Appl
865	4	33.3	412	3	US-08-465-585C-14	Sequence 14, Appl	938	4	33.3	431	1	US-08-480-528A-4	Sequence 4, Appl
866	4	33.3	412	3	US-08-652-446-14	Sequence 14, Appl	939	4	33.3	431	1	US-08-479-666-4	Sequence 4, Appl
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868	4	33.3	412	5	PCT-US91-04541-2	Sequence 2, Appl	941	4	33.3	431	1	US-08-406-672-17	Sequence 17, Appl
869	4	33.3	412	6	5262319-2	Patent No. 5262319	942	4	33.3	431	1	US-08-643-563A-17	Sequence 17, Appl
870	4	33.3	414	1	US-08-132-405-2	Sequence 2, Appl	943	4	33.3	431	1	US-08-447-570-2	Sequence 2, Appl
871	4	33.3	414	1	US-08-395-939A-2	Sequence 2, Appl	944	4	33.3	431	1	US-08-643-763A-17	Sequence 17, Appl
872	4	33.3	414	5	PCT-US91-01861-2	Sequence 2, Appl	945	4	33.3	431	1	US-08-462-623-17	Sequence 17, Appl
873	4	33.3	414	5	PCT-US94-03705-6	Sequence 6, Appl	946	4	33.3	431	1	US-08-451-953A-17	Sequence 17, Appl
874	4	33.3	414	6	5221620-4	Patent No. 5221620	947	4	33.3	431	2	US-08-459-346-2	Sequence 2, Appl
875	4	33.3	415	3	US-08-938-830-1	Sequence 1, Appl	948	4	33.3	431	2	US-08-445-468A-17	Sequence 17, Appl
876	4	33.3	415	3	US-08-020-222-1	Sequence 1, Appl	949	4	33.3	431	2	US-08-901-200A-4	Sequence 4, Appl
877	4	33.3	417	2	US-09-099-677A-6	Sequence 6, Appl	950	4	33.3	431	2	US-08-481-337A-10	Sequence 10, Appl
878	4	33.3	417	3	US-09-261-471-6	Sequence 6, Appl	951	4	33.3	431	2	US-08-449-700-2	Sequence 2, Appl
879	4	33.3	419	1	US-08-056-051-4	Sequence 4, Appl	952	4	33.3	431	2	US-07-989-847-6	Sequence 6, Appl
880	4	33.3	419	1	US-07-928-611-20	Sequence 20, Appl	953	4	33.3	431	2	US-08-449-699A-2	Sequence 2, Appl
881	4	33.3	419	2	US-08-487-811A-20	Sequence 20, Appl	954	4	33.3	431	2	US-08-696-268B-4	Sequence 4, Appl
882	4	33.3	419	4	US-09-060-694-20	Sequence 20, Appl	955	4	33.3	431	2	US-08-461-397A-17	Sequence 17, Appl
883	4	33.3	419	5	PCT-US93-07370-20	Sequence 20, Appl	956	4	33.3	431	2	US-08-912-088-17	Sequence 17, Appl
884	4	33.3	422	2	US-08-403-852D-17	Sequence 17, Appl	957	4	33.3	431	3	US-08-278-730A-17	Sequence 17, Appl
885	4	33.3	422	3	US-08-510-646B-18	Sequence 18, Appl	958	4	33.3	431	3	US-08-458-811-2	Sequence 2, Appl
886	4	33.3	422	4	US-09-231-818-17	Sequence 17, Appl	959	4	33.3	431	3	US-08-889-419-2	Sequence 2, Appl
887	4	33.3	426	1	US-08-455-550-21	Sequence 21, Appl	960	4	33.3	431	3	US-08-445-467-17	Sequence 17, Appl
888	4	33.3	426	2	US-08-644-034A-3	Sequence 3, Appl	961	4	33.3	431	3	US-08-480-515A-17	Sequence 17, Appl
889	4	33.3	427	1	US-07-958-222A-2	Sequence 2, Appl	962	4	33.3	431	3	US-08-459-129-2	Sequence 2, Appl
890	4	33.3	429	2	US-08-677-049-5	Sequence 5, Appl	963	4	33.3	431	4	US-09-219-391-4	Sequence 4, Appl
891	4	33.3	430	1	US-07-841-646-25	Sequence 25, Appl	964	4	33.3	431	4	US-08-469-411-6	Sequence 6, Appl
892	4	33.3	430	1	US-07-901-703-9	Sequence 9, Appl	965	4	33.3	431	4	US-09-019-339B-2	Sequence 2, Appl
893	4	33.3	430	1	US-08-147-023-25	Sequence 25, Appl	966	4	33.3	431	5	PCT-US90-07654-4	Sequence 4, Appl
894	4	33.3	430	1	US-08-278-729A-19	Sequence 19, Appl	967	4	33.3	431	5	PCT-US92-01968-17	Sequence 17, Appl
895	4	33.3	430	1	US-08-480-528A-6	Sequence 6, Appl	968	4	33.3	431	5	PCT-US93-05446-2	Sequence 2, Appl
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898	4	33.3	430	1	US-08-406-672-19	Sequence 19, Appl	971	4	33.3	431	5	PCT-US93-07231-17	Sequence 17, Appl
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901	4	33.3	430	1	US-08-643-763A-19	Sequence 19, Appl	974	4	33.3	431	5	PCT-US93-08885-17	Sequence 17, Appl
902	4	33.3	430	1	US-08-462-623-19	Sequence 19, Appl	975	4	33.3	431	5	PCT-US93-08885-17	Sequence 17, Appl
903	4	33.3	430	1	US-08-451-953A-19	Sequence 19, Appl	976	4	33.3	431	5	PCT-US93-08885-17	Sequence 17, Appl

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Sequence 2, Appli
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Sequence 11, Appli
Sequence 17, Appli
Sequence 11, Appli
Sequence 14, Appli
Sequence 14, Appli
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Sequence 60, Appli
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4 33.3 431 5 PCT-US93-10520-4
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4 33.3 432 2 US-08-896-005-4
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4 33.3 432 2 US-09-261-471-3
4 33.3 432 4 US-09-385-028-10
4 33.3 433 4 US-07-741-940-5
4 33.3 434 1 US-08-289-548A-5
4 33.3 434 1 US-08-452-654-5
4 33.3 434 1 US-08-452-655B-5
4 33.3 434 1 US-08-450-582-5
4 33.3 434 1 US-08-097-827-11
4 33.3 438 1 US-08-111-939-17
4 33.3 438 1 US-08-194-574-11
4 33.3 438 2 US-08-459-346-14
4 33.3 438 3 US-08-889-419-14
4 33.3 438 5 PCT-US93-07189-14
4 33.3 439 4 US-08-975-762-60
4 33.3 439 4 US-09-295-028-60
4 33.3 439 4 US-09-106-582-60

ALIGNMENTS

RESULT 1
US-08-609-090-1
; Sequence 1, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-1

Query Match 100.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
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DB 1 DAEFRHDSGYEV 12

RESULT 2
US-08-302-808-10
; Sequence 10, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-302-808-10

Query Match 100.0%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
1 DAEFRHDSGYEV 12

RESULT 3
US-08-986-948-10
; Sequence 10, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, NO. 5955317uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-986-948-10

Query Match 100.0%; Score 12; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

Db 1 DAEFRHDSGYEV 12

RESULT 4
US-08-659-984A-18
; Sequence 18, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; INHIBITION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-0028100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-18

Query Match 100.0%; Score 12; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
1 DAEFRHDSGYEV 17

RESULT 5
US-08-660-531-18
; Sequence 18, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

us-09-580-015-42_copy_1_12.oli.ra

Fri Sep 13 09:18:10 2002

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; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-660-531-18

Query Match 100.0%; Score 12; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 6 DAEFRHDSGYEV 17

RESULT 6
US-08-141-324-11
; Sequence 11, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-141-324-12

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; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-141-324-11

Query Match 100.0%; Score 12; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 9 DAEFRHDSGYEV 20

RESULT 7
US-08-141-324-12
; Sequence 12, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-141-324-12

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Query Match 100.0%; Score 12; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 9 DAEFRHDSGYEV 20
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RESULT 8
US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541.902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141.324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-541-902-11

Query Match 100.0%; Score 12; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 9 DAEFRHDSGYEV 20
|||||

RESULT 9
US-08-541-902-12

; Sequence 12, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541.902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141.324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-541-902-12

Query Match 100.0%; Score 12; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 9 DAEFRHDSGYEV 20
|||||

RESULT 10
US-08-723-661B-4
; Sequence 4, Application US/08723661B
; Patent No. 6340783
; GENERAL INFORMATION:
; APPLICANT: Alan D Snow
; TITLE OF INVENTION: Animal Models of Human Amyloidoses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrick M. Dwyer
; STREET: 1818 Westlake Avenue N, Suite 114
; CITY: Seattle
; STATE: WA (Washington)
; COUNTRY: United States of America
; ZIP: 98109

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS (Windows 98)
; SOFTWARE: WordPerfect 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,661B
; FILING DATE: 31-Oct-1996
; APPLICATION DATA:
; APPLICATION NUMBER: 08/461,216
; FILING DATE: 05-Jun-1995
; APPLICATION NUMBER: 07/969,734
; FILING DATE: 23-Oct-1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: 23-Sep-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dwyer, Patrick M.
; REGISTRATION NUMBER: 32,411
; REFERENCE/DOCKET NUMBER: PROTO.P00C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 343-7074
; TELEFAX: (206) 343-7085
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: /A4 (1-28) mutant; page 83, lines 27-28
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-723-661B-4

Query Match 100.0%; Score 12; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 11
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshio, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-9540
; TELEFAX: (617) 861-6240
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-346-849-4

Query Match 100.0%; Score 12; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 12
US-08-302-808-7
; Sequence 7, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
```

; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 US-08-302-808-7

Query Match 100.0%; Score 12; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
 Db 1 DAEFRHDSGYEV 12

RESULT 13
 US-08-609-090-2
 ; Sequence 2, Application US/08609090
 ; Patent No. 5840838
 ; GENERAL INFORMATION:
 ; APPLICANT: HENSLEY, Kenneth
 ; APPLICANT: BUTTERFIELD, D. A.
 ; APPLICANT: CARNEY, John M.
 ; APPLICANT: AKSENOV, Michael
 ; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
 ; STREET: 99 Canal Center Plaza, Suite 300
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/609,090
 ; FILING DATE: 29-FEB-1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kraus, Eric J.
 ; REGISTRATION NUMBER: 36,190
 ; REFERENCE/DOCKET NUMBER: 434-059
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-684-1111
 ; TELEFAX: 703-684-1124
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-609-090-2

Query Match 100.0%; Score 12; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12

Db 1 DAEFRHDSGYEV 12
 RESULT 14
 US-08-986-948-7
 ; Sequence 7, Application US/08986948
 ; Patent No. 5955317
 ; GENERAL INFORMATION:
 ; APPLICANT: SUZUKI, No. 5955317uhlio
 ; APPLICANT: ODAKA, Asano
 ; APPLICANT: KITADA, Chieko
 ; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
 ; DERIVATIVES AND USE THEREOF
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 ; STREET: 130 WATER STREET
 ; CITY: BOSTON
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02019
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/986,948
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/302,808
 ; FILING DATE: 15-SEP-1994
 ; APPLICATION NUMBER: PCT/JP94/00089
 ; FILING DATE: 24-JAN-1994
 ; APPLICATION NUMBER: 010132/1993
 ; FILING DATE: 25-JAN-1993
 ; APPLICATION NUMBER: 019035/1993
 ; FILING DATE: 05-FEB-1993
 ; APPLICATION NUMBER: 286985/1993
 ; FILING DATE: 16-NOV-1993
 ; APPLICATION NUMBER: 334773/1993
 ; FILING DATE: 28-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DAVID, RESNICK S
 ; REGISTRATION NUMBER: 34,235
 ; REFERENCE/DOCKET NUMBER: 44631
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; TELEX: 200291 STRE
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 US-08-986-948-7

Query Match 100.0%; Score 12; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
 Db 1 DAEFRHDSGYEV 12

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1 COUNTRY: USA
2 ZIP: 98101-2347
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
6 COMPUTER: IBM PC/386 Compatible
7 OPERATING SYSTEM: MS-DOS 4.01
8 SOFTWARE: Word for Windows-t
9
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/461,216
12 FILING DATE:
13
14 CLASSIFICATION:
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: 07/969,734
17 FILING DATE: October 23, 1992
18 APPLICATION NUMBER: 07/950,417
19 FILING DATE: September 23, 1992
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Broderick, Thomas F.
22 REGISTRATION NUMBER: 31,332
23 REFERENCE/DOCKET NUMBER: UOFW-1-6707
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
26 TELEFAX: 1-206-224-0779
27 TELEX: 4938023
28 INFORMATION FOR SEQ ID NO: 2:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 28 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: peptide
35 DESCRIPTION: {SYMBOL 98 \f "Symbol"}/A4(1-28);
36 DESCRIPTION: page 83, line 31
37
38 US-08-461-216-2
39
40
41 Query Match 100.0%; Score 12; DB 2; Length 28;
42 Best Local Similarity 100.0%; Pred.No.2.7e-07;
43 Matches 12; Conservative 0; Mismatches 0; Indels
44
45 Qy 1 DAEFRHDSGYEV 12
46 | | | | | | | | | |
47 Db 1 DAEFRHDSGYEV 12
48
49 RESULT 17
50 US-08-461-216-4
51 ; Sequence 4, Application US/08461216
52 ; Patent No. 5958883
53 ; GENERAL INFORMATION:
54 ; APPLICANT: Snow, A.D.
55 ; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
56 ; NUMBER OF SEQUENCES: 8
57 ; CORRESPONDENCE ADDRESS:
58 ; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness,
59 ; STREET: 1420 Fifth Avenue, Suite 2800
60 ; CITY: Seattle
61 ; STATE: Washington
62 ; COUNTRY: USA
63 ; ZIP: 98101-2347
64 ; COMPUTER READABLE FORM:
65 ; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
66 ; COMPUTER: IBM PC/386 Compatible
67 ; OPERATING SYSTEM: MS-DOS 4.01
68 ; SOFTWARE: Word for Windows-t
69 ; CURRENT APPLICATION DATA:
70 ; APPLICATION NUMBER: US/08/461,216
71 ; FILING DATE:
72 ; CLASSIFICATION:
73 ; PRIOR APPLICATION DATA:
74 ; APPLICATION NUMBER: 07/969,734
75 ; FILING DATE: October 23, 1992
76 ; APPLICATION NUMBER: 07/950,417
77 ;

```

;
; FILING DATE: September 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: DOW-1-6707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: {SYMBOL 98 \f "Symbol"}A4(1-28) mutant;
; DESCRIPTION: page 83, lines 27-28
US-08-461-216-4

Query Match 100.0%; Score 12; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 18
US-09-388-890-2
; Sequence 2, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:

Query Match 100.0%; Score 12; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

;
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: B(1-28) peptide of amyloid B protein
US-09-388-890-2

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 19
US-09-388-890-9
; Sequence 9, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: H13Q B(1-28) peptide of amyloid B protein
US-09-388-890-9

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

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1  ZIP: 20004
2
3  COMPUTER READABLE FORM:
4
5  MEDIUM TYPE: Floppy disk
6  COMPUTER: IBM PC compatible
7  OPERATING SYSTEM: PC-DOS/MS-DOS
8  SOFTWARE: Patentin Release #1.0, Version #1.25
9
10 CURRENT APPLICATION DATA:
11
12 APPLICATION NUMBER: US/09/388,890
13
14 FILING DATE:
15
16 CLASSIFICATION:
17
18 PRIOR APPLICATION DATA:
19
20 APPLICATION NUMBER: 08/686,959
21
22 FILING DATE:
23
24 ATTORNEY/AGENT INFORMATION:
25
26 NAME: AUERBACH, JEFFREY I.
27 REGISTRATION NUMBER: 32,680
28 TELECOMMUNICATION INFORMATION:
29
30 TELEPHONE: (202) 383-7451
31 TELEFAX: (202) 383-6610
32
33 INFORMATION FOR SEQ ID NO: 11:
34
35 SEQUENCE CHARACTERISTICS:
36
37 LENGTH: 28 amino acids
38
39 TYPE: amino acid
40
41 TOPOLOGY: linear
42
43 MOLECULE TYPE: peptide
44
45 HYPOTHETICAL: YES
46
47 FRAGMENT TYPE: N-terminal
48
49 ORIGINAL SOURCE:
50
51 ORGANISM: HOMO SAPIENS
52
53 IMMEDIATE SOURCE:
54
55 CLONE: K16Q B(1-28) peptide of amyloid B protein
56
57 US-09-388-890-11
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;
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: E22Q B(1-28) peptide of amyloid B protein
US-09-388-890-12

Query Match          100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
   | | | | | | | | | |
Db 1 DAEFRHDSGYEV 12

RESULT 23
US-09-388-890-13
; Sequence 13, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
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;
; CLONE: D23Q B(1-28) peptide of amyloid B protein
US-09-388-890-13

Query Match          100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
   | | | | | | | | | |
Db 1 DAEFRHDSGYEV 12

RESULT 24
US-09-388-890-14
; Sequence 14, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: K28Q B(1-28) peptide of amyloid B protein
US-09-388-890-14

Query Match          100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
   | | | | | | | | | |
Db 1 DAEFRHDSGYEV 12

RESULT 25
US-08-723-661B-2
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; Sequence 2, Application US/08723661B
; Patent No. 6340783
; GENERAL INFORMATION:
; APPLICANT: Alan D Snow
; TITLE OF INVENTION: Animal Models of Human Amyloidoses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrick M. Dwyer
; STREET: 1818 Westlake Avenue N, Suite 114
; CITY: Seattle
; STATE: WA (Washington)
; COUNTRY: United States of America
; ZIP: 98109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS (Windows 98)
; SOFTWARE: WordPerfect 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,661B
; FILING DATE: 31-Oct-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,216
; FILING DATE: 03-Jun-1995
; APPLICATION NUMBER: 07/969,734
; FILING DATE: 23-Oct-1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: 23-Sep-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dwyer, Patrick M.
; REGISTRATION NUMBER: 32,411
; REFERENCE/DOCKET NUMBER: PROTEO.P00C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 343-7074
; TELEFAX: (206) 343-7085
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: /A4 (1-28); page 83, line 31
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-723-661B-2

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 26
US-08-609-090-3
; Sequence 3, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-090-3

Query Match 100.0%; Score 12; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 27
US-08-609-090-4
; Sequence 4, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-090-3
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;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 33 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
US-08-609-090-4

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Query Match	100.00;	Score 12;	DB 2;	Length 33;
Best Local Similarity	100.00;	Pred. No. 3.2e-07;		

QY 1 DAEFRHDSGYEV 12
| | | | | | | | | |
Db 1 DAEFRHDSGYEV 12

RESULT 28
US-08-659-984A-16
; Sequence 16, Application US/08659984A

```

: GENERAL INFORMATION:
: APPLICANT: Anderson, John P.
: APPLICANT: Sinha, Sukanto
: APPLICANT: Jacobson-Croak, Kirsten L.
: TITLE OF INVENTION: Assays for Detecting Beta-Secretase
: TITLE OF INVENTION: Inhibition
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE:

```

;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Ctr., 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA

```

: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/659,984A
: FILING DATE: 07-JUN-1996
:

```

CLASSIFICATION: 436
PRIOR APPLICATION DATA: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PS-08-659-984A-16

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Query Match      100.0%; Score 12; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 12; Conservative 0; Mismatches 0; Indels
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Y 1 DAEFRHDSGYEV 12
b 18 DAEFRHDSGYEV 29

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RESULT 29
US-08-660-531-16
: Sequence 16, Application US/08660531
: Patent No. 6221645
: GENERAL INFORMATION:
: APPLICANT: Chrysler, Susanna M.S.
: APPLICANT: Sinha, Sukanto
: APPLICANT: Keim, Pamela S.
: APPLICANT: Anderson, John P.
: TITLE OF INVENTION: Beta-Secretase
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Ctr., 8th Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/660,531
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/480,498
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Heslin, James M.
: REGISTRATION NUMBER: 29,541
: REFERENCE/DOCKET NUMBER: 15270-002210US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 33 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: IS-08-660-531-16

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Query Match      100.0%; Score 12; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 12; Conservative 0; Mismatches 0; Indels
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QY 1 DAEFRHDSGYEV 12
| | | | | | | | | |
Db 18 DAEFRHDSGYEV 29

RESULT 30
US-08-304-585-6
; Sequence 6, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:

APPLICANT: Maggio, John E.
APPLICANT: Manlyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA

us-09-580-015-42_copy_1_12.oli.rai

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;
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-304-585-6

Query Match 100.0%; Score 12; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 31
US-08-612-785B-15
; Sequence 15, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; INFORMATION: Aggregation
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-612-785B-38

Query Match 100.0%; Score 12; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 32
US-08-612-785B-38
; Sequence 38, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; INFORMATION: Aggregation
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-612-785B-38
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Query Match 100.0%; Score 12; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 33

US-08-612-785B-39
; Sequence 39, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-39

Query Match 100.0%; Score 12; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 34

US-08-617-267C-15
; Sequence 15, Application US/08617267C

; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-15

Query Match 100.0%; Score 12; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 35

US-08-609-090-6
; Sequence 6, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA

FILING DATE: 28-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 44631
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX: 200291 STRE
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 US-08-302-808-1

Query Match 100.0%; Score 12; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 Db 1 DAEFRHDSGYEV 12

RESULT 37
 US-07-737-371E-68
 ; Sequence 68, Application US/07737371E
 ; Patent No. 5876948
 ; GENERAL INFORMATION:
 ; APPLICANT: Yankner, Bruce A.
 ; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
 ; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
 ; NUMBER OF SEQUENCES: 77
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07737,371E
 ; FILING DATE: 29-JUL-1991
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/559,172
 ; FILING DATE: 27-JUL-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Freeman, John W.
 ; REGISTRATION NUMBER: 29,066
 ; REFERENCE/DOCKET NUMBER: 00108/028002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 68:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 38 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

ZIP: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,090
 FILING DATE: 29-FEB-1996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Kraus, Eric J.
 REGISTRATION NUMBER: 36,190
 REFERENCE/DOCKET NUMBER: 434-059
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-684-1111
 TELEFAX: 703-684-1124
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 36 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-609-090-6

Query Match 100.0%; Score 12; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 Db 1 DAEFRHDSGYEV 12

RESULT 36
 US-08-302-808-1
 ; Sequence 1, Application US/08302808
 ; Patent No. 5750349
 ; GENERAL INFORMATION:
 ; APPLICANT: SUZUKI, No. 5750349uhiro
 ; APPLICANT: ODAKA, Asano
 ; APPLICANT: KITADA, Chieko
 ; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
 ; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 ; STREET: 130 WATER STREET
 ; CITY: BOSTON
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02019
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/302,808
 ; FILING DATE: 15-SEP-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/JP94/00089
 ; FILING DATE: 24-JAN-1994
 ; APPLICATION NUMBER: 010132/1993
 ; FILING DATE: 25-JAN-1993
 ; APPLICATION NUMBER: 019035/1993
 ; FILING DATE: 05-FEB-1993
 ; APPLICATION NUMBER: 286985/1993
 ; FILING DATE: 16-NOV-1993
 ; APPLICATION NUMBER: 334773/1993

; MOLECULE TYPE: protein
US-07-737-371E-68

Query Match 100.0%; Score 12; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
|||||

RESULT 38
US-08-986-948-1
; Sequence 1, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, NO. 5955317uhiro
; APPLICANT: ODARA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-986-948-1

Query Match 100.0%; Score 12; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
|||||

RESULT 39
5262332-1
; Patent No. 5262332
; APPLICANT: SELKOE, DENNIS J.
; TITLE OF INVENTION: DIAGNOSTIC METHOD FOR ALZHEIMER'S
; DISEASE: EXAMINATION OF NON-NEURAL TISSUE
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/410,138
; FILING DATE: 19-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 333,609
; FILING DATE: 05-APR-1989
; SEQ ID NO: 1:
; LENGTH: 38
5262332-1

Query Match 100.0%; Score 12; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
|||||

RESULT 40
US-08-302-808-2
; Sequence 2, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, NO. 5750349uhiro
; APPLICANT: ODARA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-7

Query Match      100.0%; Score 12; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
   | | | | | | | | | |
Db 1 DAEFRHDSGYEV 12

RESULT 42
US-08-682-245A-1
; Sequence 1, Application US/08682245A
; Patent No. 5919631
; GENERAL INFORMATION:
; APPLICANT: GOYAL, SHEFALI
; APPLICANT: PAUL, JOSEPH W
; APPLICANT: RIEDEL, NORBERT G
; APPLICANT: SAHASRABUDHE, SUDHIR
; TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
; TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOECHST MARION ROUSSEL, INC.
; STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
; CITY: CINCINNATI
; STATE: OHIO
; COUNTRY: U.S.A.
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,245A
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,414
; FILING DATE: 16-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LENTZ, NELSEN L
; REGISTRATION NUMBER: 38,537
; REFERENCE/DOCKET NUMBER: HR-1257A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-948-7369
; TELEFAX: 513-948-7961 OR 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-682-245A-1

Query Match      100.0%; Score 12; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
   | | | | | | | | | |
Db 1 DAEFRHDSGYEV 12

```

RESULT 43
US-08-986-948-2
; Sequence 2, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-986-948-2

Query Match 100.0%; Score 12; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
|||||

RESULT 44
US-07-744-767A-1

; Sequence 1, Application US/07744767A
; Patent No. 5434050
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,767A
; FILING DATE: 13-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600,226-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-744-767A-1

Query Match 100.0%; Score 12; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
|||||

RESULT 45
US-08-235-400-2
; Sequence 2, Application US/08235400
; Patent No. 5552426
; GENERAL INFORMATION:
; APPLICANT: Lunn, William H.
; APPLICANT: Monn, James A.
; APPLICANT: Zimmerman, Dennis M.
; TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
; DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

Best Local Similarity	100.0%;	Pred. No. 3.7e-07;	0;
Matches	12; Conservative	0; Mismatches	0; Gaps
		Indels	0;

Qy 1 DAEFRHDSGYEV 12
| | | | | | | | | |
Db 1 DAEFRHDSGYEV 12

RESULT 47

```

US-08-304-585-1
: Sequence 1, Application US/08304585
: Patent No. 5721106
: GENERAL INFORMATION:
: APPLICANT: Magglo, John E.
: APPLICANT: Mantyh, Patrick W.
: TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
: TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Baasch, Gebhardt & Schwappach, P.A.

```

Query Match 100.0%; Score 12; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
| | | | | | | |
Db 1 DAEFRHDSGYEV 12

RESULTS 46

```

RESOL 140
US-08-476-464A-2
; Sequence 2, Application US/08476464A
; Patent No. 5707821
; GENERAL INFORMATION:
; APPLICANT: RYDEL, RUSSELL E.
; APPLICANT: DAPPEN, MICHAEL S.
; TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
; TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
; NUMBER OF SEQUENCES: 2

```

ADDRESS: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400

TELEFAX: (415) 770 0500
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-2

Query Match
100.0%; Score 12; DB 1; Length 40;

Query Match 100.0%; Score 12; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels

QY 1 DAEFRHDSGYEV 12
| | | | | | | |
Db 1 DAEFRHDSGYEV 12

RESULT 48

RESOLUTION 40.
 US-08-304-585-8
 : Sequence 8, Application US/08304585
 : Patent No. 5721106
 : GENERAL INFORMATION:
 : APPLICANT: Maggio, John E.
 : APPLICANT: Mantyh, Patrick W.
 : TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
 : TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
 : NUMBER OF SEQUENCES: 12
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
 : STREET: P.O. Box 581415


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; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-304-585-8

Query Match 100.0%; Score 12; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
|||||

RESULT 49
US-08-302-808-3
; Sequence 3, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
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; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-302-808-3

Query Match 100.0%; Score 12; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
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RESULT 50
US-08-433-734-1
; Sequence 1, Application US/08433734
; Patent No. 5837473
; GENERAL INFORMATION:
; APPLICANT: Magglo, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; TITLE OF INVENTION: for use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,734
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1220
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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Fri Sep 13 09:18:10 2002

; MOLECULE TYPE: peptide
US-08-433-734-1

Query Match 100.0%; Score 12; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

Search completed: September 13, 2002, 09:06:06
Job time: 137 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:04:09 ; Search time 14.91 Seconds
(without alignments)
77.335 Million cell updates/sec

Title: US-09-580-015-42_COPY_1_12
Perfect score: 12
Sequence: 1 DAEFRHDSGYEV 12

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	12	100.0	42	2 PN0512	beta-amyloid prote
2	12	100.0	57	2 E60045	Alzheimer's diseas
3	12	100.0	57	2 F60045	Alzheimer's diseas
4	12	100.0	57	2 G60045	Alzheimer's diseas
5	12	100.0	57	2 D60045	Alzheimer's diseas
6	12	100.0	57	2 A60045	Alzheimer's diseas
7	12	100.0	57	2 B60045	Alzheimer's diseas
8	12	100.0	82	2 PQ0438	Alzheimer's diseas
9	12	100.0	695	1 A49795	Alzheimer's diseas
10	12	100.0	770	1 QRH044	Alzheimer's diseas
11	7	58.3	528	2 G87594	Alzheimer's diseas
12	6	50.0	122	2 S54715	Alzheimer's diseas
13	6	50.0	246	2 AG1140	Alzheimer's diseas
14	6	50.0	380	2 G69277	Alzheimer's diseas
15	6	50.0	397	2 T11786	Alzheimer's diseas
16	6	50.0	447	2 G84709	Alzheimer's diseas
17	6	50.0	453	2 C69543	Alzheimer's diseas
18	6	50.0	515	2 H86202	Alzheimer's diseas
19	6	50.0	761	2 T15776	Alzheimer's diseas
20	6	50.0	1237	2 AE1915	Alzheimer's diseas
21	6	50.0	1256	2 AB2042	Alzheimer's diseas
22	5	41.7	112	2 A86604	Alzheimer's diseas
23	5	41.7	112	2 B72019	Alzheimer's diseas
24	5	41.7	117	2 G90310	Alzheimer's diseas
25	5	41.7	123	2 H72479	Alzheimer's diseas
26	5	41.7	125	2 S68170	Alzheimer's diseas
27	5	41.7	132	2 JQ0737	Alzheimer's diseas
28	5	41.7	135	1 R3RW12	Alzheimer's diseas
29	5	41.7	135	2 A34653	Alzheimer's diseas

30	5	41.7	136	2	A87681	conserved hypothet
31	5	41.7	142	2	E89026	protein F13A2.1 [i
32	5	41.7	143	2	E90265	conserved hypothet
33	5	41.7	145	2	S62510	hypothetical prote
34	5	41.7	161	2	S30698	cyax protein - Esc
35	5	41.7	167	2	T34963	hypothetical prote
36	5	41.7	186	2	T31347	hypothetical prote
37	5	41.7	195	2	B70577	hypothetical prote
38	5	41.7	196	2	S72861	hypothetical prote
39	5	41.7	208	2	T21689	hypothetical prote
40	5	41.7	209	2	T35041	hypothetical prote
41	5	41.7	218	1	VCWZMW	coat protein - mal
42	5	41.7	219	2	C84280	ABC-type transport
43	5	41.7	220	2	B81362	probable sensory t
44	5	41.7	226	2	D83875	hypothetical prote
45	5	41.7	232	2	A13304	response regulator
46	5	41.7	234	2	A97652	two component resp
47	5	41.7	234	2	AH2875	melanoma-associate
48	5	41.7	238	1	I38016	CD63 antigen - rab
49	5	41.7	238	1	JG2297	CD63/NE491 antigen
50	5	41.7	238	1	S43511	CD63/NE491 antigen
51	5	41.7	238	1	A46508	two-component resp
52	5	41.7	239	2	E84044	hypothetical prote
53	5	41.7	239	2	T23038	transcription regu
54	5	41.7	246	2	AB1499	occM protein [impo
55	5	41.7	247	2	F98313	hypothetical prote
56	5	41.7	258	2	C84758	hypothetical prote
57	5	41.7	262	2	F95280	hypothetical prote
58	5	41.7	278	1	S74996	enoyl-lacyl-carrie
59	5	41.7	279	2	C83485	hypothetical prote
60	5	41.7	285	1	S38567	phenylethanolamine
61	5	41.7	286	2	G90482	conserved hypothet
62	5	41.7	288	2	T51059	hypothetical prote
63	5	41.7	294	2	A40993	H+/K+-exchanging A
64	5	41.7	294	2	S75521	hypothetical prote
65	5	41.7	295	2	G81724	methionine aminope
66	5	41.7	303	2	A55136	beta-coat protein
67	5	41.7	304	2	C84264	dihydroxynaphtholc
68	5	41.7	305	2	A10476	oxidative stress t
69	5	41.7	307	2	D95148	aspartate carbamoy
70	5	41.7	307	2	B98016	aspartate carbamoy
71	5	41.7	308	2	T29746	hypothetical prote
72	5	41.7	310	2	B86825	regenerating liver
73	5	41.7	314	2	A44437	transcription fact
74	5	41.7	314	2	S35314	major histocompati
75	5	41.7	317	2	A39935	Rel-associated pp4
76	5	41.7	318	2	I51192	beta-tectorin tran
77	5	41.7	323	2	E83860	hypothetical prote
78	5	41.7	329	2	A57246	conserved hypothet
79	5	41.7	331	2	S09800	hypothetical prote
80	5	41.7	336	2	G69196	arginine/ornithine
81	5	41.7	337	2	D86313	hypothetical prote
82	5	41.7	340	2	B83533	conserved hypothet
83	5	41.7	340	2	T46112	hypothetical prote
84	5	41.7	342	2	H86300	protein T16A1.7 [i
85	5	41.7	342	2	F87562	transcription regu
86	5	41.7	343	2	D71341	probable exported
87	5	41.7	346	2	T30134	hypothetical prote
88	5	41.7	350	2	AE1084	E. coli Ada protei
89	5	41.7	350	2	AE1441	E. coli Ada protei
90	5	41.7	351	2	E87451	conserved hypothet
91	5	41.7	355	2	D80065	protein T16A1.7 [i
92	5	41.7	358	2	F84053	transcription regu
93	5	41.7	385	2	T09997	lipoxigenase (EC 1
94	5	41.7	386	2	A81328	probable periplasm
95	5	41.7	392	2	G97330	probable aminopept
96	5	41.7	393	2	F75205	bacteriochlorophyl
97	5	41.7	393	2	C71240	hypothetical prote
98	5	41.7	394	2	D82725	nicotinate phospho
99	5	41.7	395	2	F82695	hypothetical prote
100	5	41.7	398	2	F83099	nicotinate phospho
101	5	41.7	399	2	E83030	nicotinate phospho
102	5	41.7	399	2	AB4972	nicotinate phospho

103	5	41.7	399	2	F89893	hypothenical prote	176	5	41.7	697	2	T00267	hypothenical prote
104	5	41.7	400	1	JQ9756	nicotinate phospho	177	5	41.7	706	2	A82091	exodeoxyribonuclea
105	5	41.7	400	1	A39130	nicotinate phospho	178	5	41.7	718	2	A82910	ppGpp 3'-pyrophosp
106	5	41.7	400	2	F90755	nicotinate phospho	179	5	41.7	739	2	A46159	interferon-depende
107	5	41.7	400	2	D85619	nicotinate phospho	180	5	41.7	758	2	E83413	hypothenical prote
108	5	41.7	400	2	AB0617	nicotinate phospho	181	5	41.7	763	2	JC4376	beta-glucosidase (
109	5	41.7	401	2	AG0172	probable nicotinat	182	5	41.7	766	2	AF2279	hypothenical prote
110	5	41.7	402	2	E81075	nicotinate phospho	183	5	41.7	774	2	AG1565	autolysin (amidase
111	5	41.7	403	2	G70038	conserved hypothet	184	5	41.7	822	2	D87325	nitrite reductase
112	5	41.7	404	2	AB1336	argininosuccinate	185	5	41.7	838	2	I45557	eyeless, long form
113	5	41.7	404	2	AH1706	argininosuccinate	186	5	41.7	838	2	T22182	hypothenical prote
114	5	41.7	404	2	E81866	nicotinate phospho	187	5	41.7	869	2	G83422	aconitate hydratase
115	5	41.7	423	2	D90927	hypothenical prote	188	5	41.7	896	2	T07408	lipoylase (EC 1
116	5	41.7	423	2	A64926	ynhC protein - Esc	189	5	41.7	898	2	S74903	DNA topoisomerase
117	5	41.7	423	2	H85775	hypothenical prote	190	5	41.7	900	2	T07062	probable lipoxigen
118	5	41.7	428	2	T27763	hypothenical prote	191	5	41.7	900	2	E83189	protein-PII uridyl
119	5	41.7	432	2	A69056	hypothenical prote	192	5	41.7	946	2	S66367	H+-transporting AT
120	5	41.7	433	2	T41038	atp-specific succi	193	5	41.7	953	2	S13520	coat protein beta
121	5	41.7	435	2	H82501	nicotinate phospho	194	5	41.7	953	2	T46913	hypothenical prote
122	5	41.7	435	2	H64693	fibronectin/fibrin	195	5	41.7	963	2	T04002	hypothenical prote
123	5	41.7	438	2	F82944	GTP-binding protei	196	5	41.7	1021	2	AC2202	hypothenical prote
124	5	41.7	439	2	F69216	conserved hypothet	197	5	41.7	1050	2	S54640	KCS1 protein - yea
125	5	41.7	441	2	G82211	response regulator	198	5	41.7	1122	2	T00441	probable histidine
126	5	41.7	442	2	T07038	probable lipoxigen	199	5	41.7	1238	2	T34929	hypothenical prote
127	5	41.7	443	2	C75617	probable oxidoredu	200	5	41.7	1292	2	A88225	protein T05H10.1 [
128	5	41.7	443	2	AF1140	hypothenical prote	201	5	41.7	1295	2	A32901	hypothenical prote
129	5	41.7	451	2	T20798	hypothenical prote	202	5	41.7	1328	2	T23007	glpI protein precu
130	5	41.7	452	2	A84262	hypothenical prote	203	5	41.7	1328	2	S66835	hypothenical prote
131	5	41.7	456	2	B96688	unknown protein, 1	204	5	41.7	1484	2	T42632	probable membrane
132	5	41.7	456	2	B84563	similar to late, em	205	5	41.7	1615	2	A49502	protein-tyrosine-p
133	5	41.7	460	2	A22009	fumarate hydratase	206	5	41.7	1687	2	T30244	phosphodiesterase
134	5	41.7	460	2	B86617	fumarate hydratase	207	5	41.7	1706	2	T30175	exoribonuclease, v
135	5	41.7	463	2	T31162	integrase homolog	208	5	41.7	1719	2	T30174	1,3-beta-glucan sy
136	5	41.7	463	2	G69829	hypothenical prote	209	5	41.7	1729	2	T43403	protein-tyrosine-p
137	5	41.7	463	2	T48116	hypothenical prote	210	5	41.7	1767	2	A49502	sucrose alpha-gluc
138	5	41.7	464	2	H90279	microtubule bindin	211	5	41.7	1841	2	T10799	hypothenical prote
139	5	41.7	465	1	F64630	cysteine--trNA lig	212	5	41.7	1908	2	T42707	genome polyprotein
140	5	41.7	465	2	D71884	cysteine--trNA lig	213	5	41.7	2127	1	ZLVNSB	genome polyprotein
141	5	41.7	467	2	T31522	hypothenical prote	214	5	41.7	2142	1	ZLVNPV	hypothenical prote
142	5	41.7	471	2	A64931	hypothenical prote	215	5	41.7	2195	2	T34264	probable RNA-direc
143	5	41.7	481	2	E86433	protein T17H7.3 [1	216	5	41.7	2517	2	S58380	fibrillin 1 - bovi
144	5	41.7	483	2	S76165	cysteine--trNA lig	217	5	41.7	2871	2	A55567	fibrillin 1 precu
145	5	41.7	486	2	E83359	chitinase PA2300 [218	5	41.7	3002	2	A47221	fibrillin 1 precu
146	5	41.7	486	2	G72358	conserved hypothet	219	5	41.7	3022	2	S79008	hypothetical 527K
147	5	41.7	486	2	D86902	hypothenical prote	220	5	41.7	4572	2	S57908	T-cell receptor al
148	5	41.7	509	2	S74935	hypothenical prote	221	5	41.7	4572	2	S57908	T-cell receptor al
149	5	41.7	517	2	A45121	alpha-1B adrenergi	222	4	33.3	11	2	S23364	type I DNA methylt
150	5	41.7	531	2	D90453	cytochrome d compl	223	4	33.3	12	2	S56122	T-cell receptor al
151	5	41.7	537	2	A38170	probable heat shoc	224	4	33.3	16	2	PH0791	hypothetical prote
152	5	41.7	539	2	T39150	hypothetical prote	225	4	33.3	31	2	C82851	beta-amyloid prote
153	5	41.7	560	2	T29586	hypothetical prote	226	4	33.3	33	2	S23094	neuropeptide F - b
154	5	41.7	565	2	T16408	5'-nucleotidase (E	227	4	33.3	39	2	A48544	gene 67 protein -
155	5	41.7	574	1	S11032	glycoprotein E - s	228	4	33.3	43	2	S31012	hypothetical prote
156	5	41.7	577	1	VGBEG1	hypothetical prote	229	4	33.3	52	2	C91112	unknown protein en
157	5	41.7	604	2	S55270	catrocollastatin p	230	4	33.3	53	2	E85716	hypothetical prote
158	5	41.7	609	2	S55270	hypothetical prote	231	4	33.3	53	2	G97845	truncated transpos
159	5	41.7	611	2	AT0592	hypothetical prote	232	4	33.3	57	2	B89981	hypothetical prote
160	5	41.7	614	2	AT2882	hypothetical prote	233	4	33.3	58	2	D69449	probable preprotei
161	5	41.7	620	2	AG1598	MFS permease [suga	234	4	33.3	59	2	E71349	hypothetical prote
162	5	41.7	625	2	D86244	internalin like pr	235	4	33.3	60	2	D84173	hypothetical prote
163	5	41.7	632	2	C90932	protein Ser/Thr pr	236	4	33.3	61	2	H82090	toxin IV-5 - Tityu
164	5	41.7	632	2	G85780	hypothetical prote	237	4	33.3	62	2	S62863	hypothetical prote
165	5	41.7	635	2	F90551	lipoprotein [impor	238	4	33.3	62	2	H89941	M protein precuso
166	5	41.7	636	2	JA0047	class I cyto kinase	239	4	33.3	63	2	S60850	peth protein - Syn
167	5	41.7	647	2	S84871	probable membrane	240	4	33.3	63	2	E82480	hypothetical prote
168	5	41.7	649	1	JH0261	parasporal crystal	241	4	33.3	64	2	E69172	sensory transducti
169	5	41.7	652	2	T23733	parasporal crystal	242	4	33.3	64	2	T30785	hypothetical prote
170	5	41.7	655	2	T35975	probable acyl-pept	243	4	33.3	65	2	S10561	chlorophyll a/b-bi
171	5	41.7	657	2	G97658	hypothetical prote	244	4	33.3	66	2	E70083	hypothetical prote
172	5	41.7	660	2	T21551	hypothetical prote	245	4	33.3	66	2	T40218	probable ATP synth
173	5	41.7	687	2	E87275	TonB-dependent rec	246	4	33.3	67	2	AT1594	hypothetical prote
174	5	41.7	693	1	S61067	homoaconitate hydr	247	4	33.3	67	2	AD1306	probable mercuric
175	5	41.7	693	2	AT0996	4-alpha-glucanotra	248	4	33.3	68	2	AD1306	probable mercuric

249	4	33.3	68	2	AD1678	probable mercuric	322	4	33.3	98	2	S06671	cinnamomin - Phyto
250	4	33.3	69	2	C84275	hypothetical prote	323	4	33.3	98	2	A82503	hypothetical prote
251	4	33.3	69	2	AG2563	hypothetical prote	324	4	33.3	98	2	AI1774	Ig heavy chain V r
252	4	33.3	69	2	AH3440	cold shock protein	325	4	33.3	99	2	S24259	collagen alpha 2(I
253	4	33.3	71	2	T42025	hypothetical prote	326	4	33.3	99	2	B38623	capsicein - Phytop
254	4	33.3	71	2	T39627	hypothetical prote	327	4	33.3	99	2	S42360	preproteins translo
255	4	33.3	72	2	H83333	hypothetical prote	328	4	33.3	99	2	E95237	conserved hypoteth
256	4	33.3	72	2	E69386	hypothetical prote	329	4	33.3	99	2	F98101	conserved hypoteth
257	4	33.3	73	2	G95106	hypothetical prote	330	4	33.3	100	2	AI2298	phd protein - phag
258	4	33.3	73	2	S40015	hypothetical prote	331	4	33.3	100	2	AB2945	hypothetical prote
259	4	33.3	73	2	S04874	hypothetical prote	332	4	33.3	100	2	AB2945	hypothetical prote
260	4	33.3	74	2	AH1317	ferredoxin homolog	333	4	33.3	101	2	D75013	hypothetical prote
261	4	33.3	74	2	AH1689	ferredoxin homolog	334	4	33.3	101	2	AF2830	hypothetical prote
262	4	33.3	76	2	A99817	hypothetical prote	335	4	33.3	101	2	E84561	hypothetical prote
263	4	33.3	76	2	D54252	hypothetical prote	336	4	33.3	103	2	AD1778	hypothetical prote
264	4	33.3	76	2	B54252	omega-agatoxin III	337	4	33.3	103	2	AE1402	ribosomal protein
265	4	33.3	76	2	B54252	omega-agatoxin III	338	4	33.3	103	2	T03013	hypothetical prote
266	4	33.3	76	2	E85676	unknown protein en	339	4	33.3	103	2	AG0570	hypothetical prote
267	4	33.3	77	2	F69219	conserved hypoteth	340	4	33.3	104	2	S04719	ribosomal protein
268	4	33.3	77	2	E31685	EFC protein - fowl	341	4	33.3	104	2	S49803	hypothetical prote
269	4	33.3	77	2	T47296	hypothetical prote	342	4	33.3	104	2	C97608	hypothetical prote
270	4	33.3	80	1	NTSR4T	hypothetical prote	343	4	33.3	104	2	A82154	hypothetical prote
271	4	33.3	81	2	S28041	neurotoxin tsiv pr	344	4	33.3	105	2	T06085	probable auxin-ind
272	4	33.3	81	2	D95065	conserved domain p	345	4	33.3	105	2	T37632	hypothetical prote
273	4	33.3	81	2	B84353	hypothetical prote	346	4	33.3	105	2	F83515	hypothetical prote
274	4	33.3	81	2	E97932	hypothetical prote	347	4	33.3	105	2	C97828	hypothetical prote
275	4	33.3	82	2	AH0205	hypothetical prote	348	4	33.3	105	2	AD2301	hypothetical prote
276	4	33.3	82	2	AB0272	hypothetical prote	349	4	33.3	106	2	T16377	hypothetical prote
277	4	33.3	83	2	D87676	hypothetical prote	350	4	33.3	106	2	G72059	hypothetical prote
278	4	33.3	84	2	S71290	hypothetical prote	351	4	33.3	106	2	D86563	conserved hypoteth
279	4	33.3	84	2	H65092	retrovirus-related	352	4	33.3	106	2	T42698	hypothetical prote
280	4	33.3	84	2	S43801	conserved hypoteth	353	4	33.3	106	2	AG2867	hypothetical prote
281	4	33.3	84	2	G96025	hypothetical prote	354	4	33.3	107	2	AI2511	hypothetical prote
282	4	33.3	84	2	AE2007	hypothetical prote	355	4	33.3	107	2	C83830	transcription regu
283	4	33.3	85	2	T47563	hypothetical prote	356	4	33.3	107	2	H98337	hypothetical prote
284	4	33.3	85	2	E97348	kinetochores-like p	357	4	33.3	108	2	D69124	hypothetical prote
285	4	33.3	86	2	C97514	heavy-metal bindin	358	4	33.3	108	2	H65012	ribosomal protein
286	4	33.3	86	2	AT2732	hypothetical prote	359	4	33.3	108	2	C91037	probable PTS syste
287	4	33.3	87	1	JH0142	conserved hypoteth	360	4	33.3	108	2	E85881	probable PTS syste
288	4	33.3	87	1	ZGBPT9	3',5'-cyclic-GMP p	361	4	33.3	108	2	E84217	hypothetical prote
289	4	33.3	87	1	ZGBPT9	gene 55.1 protein	362	4	33.3	109	2	S77444	hypothetical prote
290	4	33.3	88	2	D98021	degenerate transpo	363	4	33.3	109	2	B64145	hypothetical prote
291	4	33.3	88	2	T14851	reverse transcript	364	4	33.3	109	2	S33836	hypothetical prote
292	4	33.3	88	2	T14859	reverse transcript	365	4	33.3	109	2	D82994	hypothetical prote
293	4	33.3	88	2	T14860	reverse transcript	366	4	33.3	109	2	C97807	hypothetical prote
294	4	33.3	88	2	T14944	hypothetical prote	367	4	33.3	110	2	D87498	hypothetical prote
295	4	33.3	88	2	C97201	probable metal-bin	368	4	33.3	111	1	A32233	thioredoxin 2 [val
296	4	33.3	89	2	S10002	hypothetical prote	369	4	33.3	111	2	T26863	thioredoxin 2 [val
297	4	33.3	89	2	D84414	hypothetical prote	370	4	33.3	112	1	S16193	tRNA (uracil-5-)-m
298	4	33.3	89	2	C82331	hypothetical prote	371	4	33.3	112	2	PH0979	ferredoxin [2Fe-2S
299	4	33.3	89	2	G97365	hypothetical prote	372	4	33.3	113	2	SI1901	Ig heavy chain V r
300	4	33.3	91	2	T16095	hypothetical prote	373	4	33.3	113	2	SI1901	hypothetical prote
301	4	33.3	91	2	S61907	protein YCR054c ho	374	4	33.3	114	2	F71018	hypothetical prote
302	4	33.3	92	2	AC9378	hypothetical prote	375	4	33.3	114	2	D64345	hypothetical prote
303	4	33.3	92	2	A99973	hypothetical prote	376	4	33.3	114	2	A72734	hypothetical prote
304	4	33.3	92	2	D83138	hypothetical prote	377	4	33.3	115	2	AF2098	hypothetical prote
305	4	33.3	93	2	G91002	hypothetical prote	378	4	33.3	115	2	B25387	thioredoxin 2 [imp
306	4	33.3	94	2	B86195	hypothetical prote	379	4	33.3	115	2	S69297	thioredoxin 2 [imp
307	4	33.3	94	2	A83633	hypothetical prote	380	4	33.3	115	2	T31584	probable membrane
308	4	33.3	94	2	S74531	hypothetical prote	381	4	33.3	115	2	E84340	hypothetical prote
309	4	33.3	94	2	S23685	hypothetical prote	382	4	33.3	115	2	E97483	hypothetical prote
310	4	33.3	94	2	T27370	hypothetical prote	383	4	33.3	115	2	T50390	hypothetical prote
311	4	33.3	94	2	E98468	hypothetical prote	384	4	33.3	116	2	A72763	hypothetical prote
312	4	33.3	95	1	A46313	hypothetical prote	385	4	33.3	116	2	E70510	hypothetical prote
313	4	33.3	96	2	S38916	hypothetical prote	386	4	33.3	116	2	B89964	hypothetical prote
314	4	33.3	97	1	RCBP22	hypothetical protei	387	4	33.3	117	2	A83312	truncated transpos
315	4	33.3	97	1	H84901	hypothetical prote	388	4	33.3	117	2	G90464	conserved hypoteth
316	4	33.3	97	2	F83200	conserved hypoteth	389	4	33.3	117	2	T35913	hypothetical prote
317	4	33.3	97	2	T25074	hypothetical prote	390	4	33.3	118	2	S49913	hypothetical prote
318	4	33.3	97	2	G82725	conserved hypoteth	391	4	33.3	118	2	S49905	cryptogeiin - Phyto
319	4	33.3	97	2	G97876	degenerate transpo	392	4	33.3	118	2	D97046	acidic elicitor A1
320	4	33.3	98	2	S03491	T-cell receptor be	393	4	33.3	118	2	D89872	hypothetical prote
321	4	33.3	98	2	S26932	Ig heavy chain V r	394	4	33.3	119	2	C25114	conserved hypoteth
	4	33.3	98	2	S05527	capsicein - Phytop		4	33.3	119	2	E81162	conserved hypoteth

395	4	33.3	119	2	H71610	hypothenical prote	468	4	33.3	132	2	T09626	outer membrane pro
396	4	33.3	119	2	T17032	fimbriata-associat	469	4	33.3	132	2	PC4020	degenerate 132 p
397	4	33.3	119	2	G97358	rnpA, ribonuclease	470	4	33.3	132	2	E98006	hypothetical transp
398	4	33.3	119	2	AB1852	transposase all036	471	4	33.3	133	2	A82955	hypothetical prote
399	4	33.3	119	2	AD2038	transposase alr185	472	4	33.3	133	2	E8796	arsenate reductase
400	4	33.3	120	2	AC2286	NADH dehydrogenase	473	4	33.3	133	2	F97362	PTS enzyme IIA, m
401	4	33.3	120	2	B72346	chemotaxis respon	474	4	33.3	133	2	AH2580	PTS system, IIA, co
402	4	33.3	120	2	H95223	hypothetical prote	475	4	33.3	134	2	A82455	hypothetical prote
403	4	33.3	120	2	C98088	hypothetical prote	476	4	33.3	134	2	G82477	hypothetical prote
404	4	33.3	120	2	F72586	hypothetical prote	477	4	33.3	134	2	B86720	conserved hypoteth
405	4	33.3	121	2	I40652	RNase P protein co	478	4	33.3	135	2	SL7081	T-cell receptor al
406	4	33.3	121	2	D83624	probable two-compo	479	4	33.3	135	2	G97856	hypothetical prote
407	4	33.3	121	2	AF1922	two-component syst	480	4	33.3	136	2	B56338	phospholipase A2 (
408	4	33.3	121	2	S69909	Ig V-D-J region (M	481	4	33.3	136	2	T17095	RNA-directed DNA p
409	4	33.3	122	2	D72374	response regulator	482	4	33.3	136	2	T13388	hypothetical prote
410	4	33.3	122	2	A97564	hypothetical prote	483	4	33.3	136	2	T17621	hypothetical prote
411	4	33.3	122	2	AH2784	conserved hypoteth	484	4	33.3	137	2	T32161	hypothetical prote
412	4	33.3	123	2	PC4281	anti-SS-A/Ro 60K p	485	4	33.3	137	2	C84198	hypothetical prote
413	4	33.3	123	2	S75663	sensory transducti	486	4	33.3	138	2	T13557	hypothetical prote
414	4	33.3	123	2	AB3592	two component resp	487	4	33.3	138	2	AE1968	hypothetical prote
415	4	33.3	123	2	S70248	hypothetical prote	488	4	33.3	138	2	F72621	hypothetical prote
416	4	33.3	123	2	S70243	hypothetical prote	489	4	33.3	138	2	S34360	hypothetical 15.8K
417	4	33.3	123	2	AD1985	HesB protein (impo	490	4	33.3	138	2	S56480	hypothetical prote
418	4	33.3	123	2	S29304	hypothetical prote	491	4	33.3	138	2	H91282	hypothetical prote
419	4	33.3	123	2	S49906	HAE (highly acidic	492	4	33.3	138	2	B86124	conserved hypoteth
420	4	33.3	123	2	E95240	HAE (highly acidic	493	4	33.3	138	2	AE1060	hypothetical prote
421	4	33.3	123	2	E95240	conserved hypoteth	494	4	33.3	138	2	S75128	hypothetical prote
422	4	33.3	123	2	F98104	conserved hypoteth	495	4	33.3	138	2	B70867	transcription regu
423	4	33.3	123	2	D84161	hypothetical prote	496	4	33.3	138	2	AB1306	hypothetical prote
424	4	33.3	123	2	G95878	probable Tm2011-2	497	4	33.3	139	1	F64502	gp70 protein - Myc
425	4	33.3	124	2	S66696	probable membrane	498	4	33.3	139	2	F72808	lysozyme (EC 3.2.1
426	4	33.3	124	2	H82117	hypothetical prote	499	4	33.3	140	2	UC5003	3C.16c protein -
427	4	33.3	124	2	B87345	hypothetical prote	500	4	33.3	140	2	T10925	hypothetical prote
428	4	33.3	125	2	S37455	Ig mu chain - huma	501	4	33.3	140	2	AH1517	En/Spm-like transp
429	4	33.3	125	2	C97286	ribosomal protein	502	4	33.3	140	2	G84608	transcription regu
430	4	33.3	125	2	B87322	chemotaxis protein	503	4	33.3	140	2	AB1678	transcription regu
431	4	33.3	125	2	D82380	gene e8 protein -	504	4	33.3	141	2	T17540	endonuclease V-lik
432	4	33.3	125	2	S54062	hypothetical prote	505	4	33.3	141	2	S54236	Ig mu heavy chain
433	4	33.3	126	2	B95111	lactylglutathione	506	4	33.3	141	2	T42177	probable antirestre
434	4	33.3	126	2	F70910	hypothetical prote	507	4	33.3	141	2	H72693	hypothetical prote
435	4	33.3	127	2	T23443	hypothetical prote	508	4	33.3	141	2	D85605	unknown in ISEc8 (
436	4	33.3	127	2	G87013	hypothetical prote	509	4	33.3	141	2	G85662	unknown protein pr
437	4	33.3	127	2	AH2860	hypothetical prote	510	4	33.3	141	2	A99796	hypothetical prote
438	4	33.3	127	2	G97637	conserved hypoteth	511	4	33.3	141	2	A99803	hypothetical prote
439	4	33.3	127	2	A84791	hypothetical prote	512	4	33.3	141	2	T38771	hypothetical prote
440	4	33.3	128	2	C69488	hypothetical prote	513	4	33.3	142	2	AH1158	hypothetical prote
441	4	33.3	128	2	S75259	LSU ribosomal prot	514	4	33.3	142	2	AH1501	hypothetical prote
442	4	33.3	129	2	B35216	Fp14 protein - fow	515	4	33.3	142	2	A87501	hypothetical prote
443	4	33.3	129	2	C97746	hypothetical prote	516	4	33.3	142	2	H95310	3-dehydroquinat d
444	4	33.3	129	2	F95062	hypothetical prote	517	4	33.3	142	2	H97590	hypothetical prote
445	4	33.3	129	2	G95108	IS1381, transposas	518	4	33.3	143	2	F71641	hypothetical prote
446	4	33.3	129	2	E95125	IS1381, transposas	519	4	33.3	143	2	H69897	hypothetical prote
447	4	33.3	129	2	F95138	IS1381, transposas	520	4	33.3	143	2	T15669	hypothetical prote
448	4	33.3	129	2	C95225	IS1381, transposas	521	4	33.3	143	2	AG0418	conserved hypoteth
449	4	33.3	129	2	C95243	IS1381, transposas	522	4	33.3	143	2	B84459	hypothetical prote
450	4	33.3	129	2	B95250	IS1381, transposas	523	4	33.3	143	2	H83935	hypothetical prote
451	4	33.3	129	2	T34674	hypothetical prote	524	4	33.3	143	2	H97979	hypothetical prote
452	4	33.3	129	2	A97977	transposase (orf2)	525	4	33.3	144	2	D11335	lactoylglutathione
453	4	33.3	129	2	B97996	transposase (orf2)	526	4	33.3	144	2	F71685	probable chemotaxi
454	4	33.3	129	2	C98068	transposase (orf2)	527	4	33.3	144	2	B97750	galactose-6-phosph
455	4	33.3	129	2	H98107	transposase (orf2)	528	4	33.3	144	2	T12102	ribose-5-phosphate
456	4	33.3	129	2	H98114	transposase (orf2)	529	4	33.3	144	2	D45691	glycine-rich prote
457	4	33.3	129	2	E45893	transposase (orf2)	530	4	33.3	144	2	D45691	hypothetical prote
458	4	33.3	130	2	D71185	T-cell receptor al	531	4	33.3	144	2	H81823	hypothetical prote
459	4	33.3	130	2	G75145	probable ribosomal	532	4	33.3	144	2	AB2443	hypothetical prote
460	4	33.3	130	2	B61942	lsu ribosomal prot	533	4	33.3	144	2	B95242	conserved hypoteth
461	4	33.3	130	2	T29887	hypothetical prote	534	4	33.3	144	2	E98106	3-dehydroquinat d
462	4	33.3	130	2	T20334	hypothetical prote	535	4	33.3	144	2	AD2740	G10 protein homolo
463	4	33.3	131	2	A11964	hypothetical prote	536	4	33.3	145	2	T04942	hypothetical prote
464	4	33.3	131	2	S23374	hypothetical prote	537	4	33.3	145	2	C72668	probable periplasm
465	4	33.3	132	2	E90583	30S ribosomal prot	538	4	33.3	145	2	G81263	hypothetical prote
466	4	33.3	132	2	H87565	hypothetical prote	539	4	33.3	145	2	T139564	hypothetical prote
467	4	33.3	132	2	H87565	hypothetical prote	540	4	33.3	145	2		

541	4	33.3	146	2	G75215	methylmalonyl-coa	614	4	33.3	160	2	C72501	hypothetical prote
542	4	33.3	146	2	AD2257	transposase air361	615	4	33.3	160	2	F72503	hypothetical prote
543	4	33.3	146	2	AE2142	transposase air269	616	4	33.3	160	2	A84104	hypothetical prote
544	4	33.3	146	2	AF2450	transposase air515	617	4	33.3	161	2	H86961	probable antioxi
545	4	33.3	146	2	AG1808	transposase all001	618	4	33.3	161	2	B91221	hypothetical prote
546	4	33.3	146	2	AG2355	transposase all439	619	4	33.3	161	2	D86067	hypothetical prote
547	4	33.3	146	2	AG2360	transposase air443	620	4	33.3	161	2	S04765	LAT52 protein prec
548	4	33.3	146	2	AH2407	transposase all481	621	4	33.3	161	2	A31901	lincomycin resista
549	4	33.3	146	2	A86490	protein r32E20.11	622	4	33.3	161	2	T48285	hypothetical prote
550	4	33.3	146	2	S14884	hypothetical prote	623	4	33.3	161	2	E87455	conserved hypotet
551	4	33.3	147	2	D71452	probable methylmal	624	4	33.3	161	2	T16207	hypothetical prote
552	4	33.3	147	2	T04470	probable trypsin i	625	4	33.3	161	2	B86421	hypothetical prote
553	4	33.3	147	2	S74986	regulatory compone	626	4	33.3	162	2	B97521	FI18.18 protein -
554	4	33.3	147	2	S75581	hypothetical prote	627	4	33.3	162	2	F97505	3-dehydroquinat
555	4	33.3	147	2	T09972	hypothetical prote	628	4	33.3	162	2	D83073	heavy metal depend
556	4	33.3	148	1	FXDV	flavodoxin - desul	629	4	33.3	162	2	AB2724	transcription regu
557	4	33.3	148	2	B6960	3-dehydroquinat	630	4	33.3	162	2	B82350	conserved hypotet
558	4	33.3	148	2	F75091	hypothetical prote	631	4	33.3	162	2	T40004	conserved hypotet
559	4	33.3	148	2	AH1166	hypothetical prote	632	4	33.3	162	2	T44758	hypothetical prote
560	4	33.3	149	2	G70069	hypothetical prote	633	4	33.3	162	2	D70721	hypothetical prote
561	4	33.3	149	2	T16551	poly-gamma-glutami	634	4	33.3	164	2	S21830	hypothetical prote
562	4	33.3	149	2	T03477	hypothetical prote	635	4	33.3	164	2	H65086	apolipoprotein A-I
563	4	33.3	150	1	MC2P	potential phosphat	636	4	33.3	164	2	F91114	hypothetical prote
564	4	33.3	150	2	A59103	calmodulin - fissi	637	4	33.3	164	2	F85959	hypothetical prote
565	4	33.3	150	2	A93633	hypothetical prote	638	4	33.3	164	2	A10885	hypothetical prote
566	4	33.3	150	2	G84585	hypothetical prote	639	4	33.3	164	2	S75684	probable membrane
567	4	33.3	150	2	F95959	hypothetical kinetech	640	4	33.3	164	2	F95958	hypothetical prote
568	4	33.3	150	2	A11968	hypothetical membr	641	4	33.3	165	2	S95899	conserved hypotet
569	4	33.3	150	2	T00839	hypothetical prote	642	4	33.3	165	2	S73371	chlorocruorin chal
570	4	33.3	151	2	AC0407	hypothetical prote	643	4	33.3	165	2	B97354	hypothetical prote
571	4	33.3	151	2	C64392	ribose-5-phosphate	644	4	33.3	165	2	A69174	hypothetical prote
572	4	33.3	151	2	A69539	hypothetical prote	645	4	33.3	166	2	S71209	hypothetical prote
573	4	33.3	151	2	A64038	hypothetical prote	646	4	33.3	166	2	T45703	ubiquitin--protein
574	4	33.3	151	2	T34245	hypothetical prote	647	4	33.3	166	2	A28127	ubiquitin--protein
575	4	33.3	151	2	AF2532	hypothetical prote	648	4	33.3	166	2	D89977	myosin light chain
576	4	33.3	152	2	D75367	hypothetical prote	649	4	33.3	167	1	RSQDF	dihydrofolate redu
577	4	33.3	152	2	MYK49	hypothetical prote	650	4	33.3	167	2	H83784	VP29-like phosph
578	4	33.3	153	1	H70459	hypothetical prote	651	4	33.3	167	2	S46566	ubiquitin--protein
579	4	33.3	153	2	S54841	myoglobin - red ka	652	4	33.3	167	2	T22198	hypothetical prote
580	4	33.3	153	2	PQ0255	peptidylprolyl iso	653	4	33.3	168	2	E64367	probable small hea
581	4	33.3	153	2	A95928	polyprotein (clone	654	4	33.3	168	2	A31770	hypothetical prote
582	4	33.3	153	2	T09405	probable amine oxi	655	4	33.3	168	2	T14723	pheromone-binding
583	4	33.3	153	2	B84036	conserved hypotet	656	4	33.3	168	2	B64397	antirestriction pr
584	4	33.3	153	2	D71131	hypothetical prote	657	4	33.3	169	2	E87657	hypothetical prote
585	4	33.3	154	2	T39021	hypothetical prote	658	4	33.3	170	1	HMECBM	hypothetical prote
586	4	33.3	154	2	T47825	hypothetical prote	659	4	33.3	170	2	D69131	M-agglutinin precu
587	4	33.3	154	2	T46006	Skp1-like protein	660	4	33.3	170	2	B64713	tRNA intron endonu
588	4	33.3	155	2	S21659	hypothetical prote	661	4	33.3	170	2	T24463	hypothetical prote
589	4	33.3	155	2	AE0534	ribonuclease H [im	662	4	33.3	170	2	T02707	hypothetical prote
590	4	33.3	155	2	H81363	ribonuclease H [EC	663	4	33.3	170	2	H84752	probable kinetech
591	4	33.3	155	2	T35458	probable RNA methy	664	4	33.3	170	2	T08348	probable DOF zinc
592	4	33.3	155	2	A12450	hypothetical prote	665	4	33.3	171	2	B39778	hypothetical prote
593	4	33.3	155	2	AB1545	hypothetical prote	666	4	33.3	171	2	S27702	galactose-6-phosph
594	4	33.3	155	2	AC1187	B. subtilis ydcK p	667	4	33.3	171	2	D43258	galactose-6-phosph
595	4	33.3	156	2	T02166	B. subtilis ydcK p	668	4	33.3	171	2	D95138	galactose-6-phosph
596	4	33.3	156	2	B64036	cysteine proteinas	669	4	33.3	171	2	B98006	hypothetical prote
597	4	33.3	156	2	T36755	hypothetical prote	670	4	33.3	171	2	T32886	galactose-6-phosph
598	4	33.3	157	2	D75151	probable acetyltra	671	4	33.3	172	2	A95370	galactose-6-phosph
599	4	33.3	157	2	H69849	hypothetical prote	672	4	33.3	172	2	H81251	galactose-6-phosph
600	4	33.3	157	2	G84292	hypothetical prote	673	4	33.3	172	2	AI0899	hypothetical prote
601	4	33.3	157	2	F83709	hypothetical prote	674	4	33.3	172	2	T10346	hypothetical prote
602	4	33.3	158	1	A38148	hypothetical prote	675	4	33.3	172	2	AE2857	transcription anti
603	4	33.3	158	2	S37355	protein-tyrosine-p	676	4	33.3	172	2	E71166	hypothetical prote
604	4	33.3	158	2	B69494	glutamate--ammonia	677	4	33.3	172	2	G97287	conserved hypotet
605	4	33.3	158	2	A54612	hypothetical prote	678	4	33.3	173	2	C97634	hypothetical prote
606	4	33.3	158	2	H71902	conserved hypotet	679	4	33.3	173	2	AE2857	transcription anti
607	4	33.3	158	2	AB3299	phosphatidylglycer	680	4	33.3	173	2	E71166	hypothetical prote
608	4	33.3	159	1	E71208	hypothetical prote	681	4	33.3	174	2	S55597	hypothetical prote
609	4	33.3	159	2	H83279	hypothetical prote	682	4	33.3	174	2	G72381	hypothetical prote
610	4	33.3	160	2	AI1308	hypothetical prote	683	4	33.3	174	2	G89981	hypothetical prote
611	4	33.3	160	2	AI1680	dihydrofolate redu	684	4	33.3	174	2	H84999	hypothetical prote
612	4	33.3	160	2	T45939	dihydrofolate redu	685	4	33.3	174	2	AI0618	chaperone protein
613	4	33.3	160	2	F87307	spoU rRNA methylas	686	4	33.3	174	2		conserved hypotet

687	4	33.3	174	2	AB3296	deoxyuridine 5'-tr	760	4	33.3	187	2	T45176	conserved hypothet
688	4	33.3	175	1	G69518	isochorismatase (e	761	4	33.3	187	2	S43177	p18 protein - Leis
689	4	33.3	176	2	PQ0253	polyprotein (clone	762	4	33.3	187	2	S36918	zygote-specific pr
690	4	33.3	175	2	D75467	bacterioferritin c	763	4	33.3	187	2	S00837	mcgB protein - Esc
691	4	33.3	175	2	H87377	conserved hypothet	764	4	33.3	187	2	H75489	hypothetical prote
692	4	33.3	175	2	G84383	hypothetical prote	765	4	33.3	187	2	E86478	protein F1504.9 [l
693	4	33.3	175	2	S71884	hypothetical prote	766	4	33.3	187	2	A71328	probable survival
694	4	33.3	176	2	H72201	conserved hypothet	767	4	33.3	188	2	A71328	adrenomedullin - p
695	4	33.3	176	2	JK0226	arachin 21k chain	768	4	33.3	188	2	S41600	hypothetical prote
696	4	33.3	176	2	T46709	hypothetical prote	769	4	33.3	188	2	A75392	hypothetical prote
697	4	33.3	176	2	D95322	hypothetical prote	770	4	33.3	189	2	A31348	hypothetical prote
698	4	33.3	176	2	AD1613	hypothetical prote	771	4	33.3	189	2	D75339	hypothetical prote
699	4	33.3	176	2	AH1250	hypothetical prote	772	4	33.3	189	2	H70875	tryptophan repress
700	4	33.3	177	1	S74917	adenylsulfate ki	773	4	33.3	190	2	D82719	NADH dehydrogenase
701	4	33.3	177	2	T31086	probable drpp-4-de	774	4	33.3	190	2	T12155	translation elonga
702	4	33.3	177	2	A31204	eggshell protein p	775	4	33.3	190	2	S73451	conserved hypothet
703	4	33.3	177	2	D83111	transcription anti	776	4	33.3	190	2	T08238	hypothetical prote
704	4	33.3	177	2	S39859	transcription anti	777	4	33.3	190	2	T32265	hypothetical prote
705	4	33.3	177	2	AG1105	transcription anti	778	4	33.3	191	1	F69187	epoxidase - Methan
706	4	33.3	177	2	AG1467	transcription anti	779	4	33.3	191	1	B65022	yifH protein - Esc
707	4	33.3	177	2	G84189	hypothetical prote	780	4	33.3	191	2	T31594	hypothetical prote
708	4	33.3	177	2	C87468	response regulator	781	4	33.3	191	2	A91045	hypothetical prote
709	4	33.3	177	2	F95912	hypothetical prote	782	4	33.3	191	2	C86840	hypothetical prote
710	4	33.3	177	2	AB3649	hypothetical prote	783	4	33.3	191	2	E75132	molybdopterin-guan
711	4	33.3	178	2	F83664	transcription anti	784	4	33.3	191	2	E75132	hypothetical prote
712	4	33.3	178	2	A95235	transcription anti	785	4	33.3	192	2	G81301	hypothetical prote
713	4	33.3	178	2	C69996	hypothetical prote	786	4	33.3	192	2	C90076	MdaB protein homol
714	4	33.3	178	2	AF1368	B. subtilis ytm1 p	787	4	33.3	192	2	T13225	amidotransferase h
715	4	33.3	178	2	AG1737	B. subtilis ytm1 p	788	4	33.3	192	2	T13225	hypothetical prote
716	4	33.3	178	2	B87104	conserved hypothet	789	4	33.3	192	2	F72338	conserved hypothet
717	4	33.3	178	2	T44823	probable macrophag	790	4	33.3	192	2	B96837	hypothetical prote
718	4	33.3	179	2	S62019	hypothetical prote	791	4	33.3	192	2	A11978	hypothetical prote
719	4	33.3	179	2	T42293	hypothetical prote	792	4	33.3	192	2	A72646	hypothetical prote
720	4	33.3	179	2	H87667	atp synthase delta	793	4	33.3	192	2	G71089	hypothetical prote
721	4	33.3	179	2	E90545	hypoxanthine phosph	794	4	33.3	192	2	F82645	insulin-like growt
722	4	33.3	180	2	G98283	hypoxanthine phosph	795	4	33.3	193	2	A53697	probable hydrolase
723	4	33.3	180	2	AB3000	hypothetical prote	796	4	33.3	193	2	S36285	DNA-3-methyladenin
724	4	33.3	180	2	T44944	hypothetical prote	797	4	33.3	193	2	A49704	transcription init
725	4	33.3	180	2	F83758	chromate transport	798	4	33.3	193	2	AF2966	anthranilate synth
726	4	33.3	180	2	F97149	probable flavodoxi	799	4	33.3	194	2	F71836	beta 8 integrin -
727	4	33.3	181	2	A69077	conserved hypothet	800	4	33.3	194	2	A64680	holliday junction
728	4	33.3	181	2	B82077	ampD protein VC242	801	4	33.3	194	2	I51310	heat-shock protein
729	4	33.3	181	2	AE3600	hypothetical prote	802	4	33.3	194	2	G82623	conserved hypothet
730	4	33.3	181	2	S73534	hypothetical prote	803	4	33.3	194	2	A75515	RNA polymerase sig
731	4	33.3	182	2	E64678	NADH dehydrogenase	804	4	33.3	194	2	G87453	hypothetical prote
732	4	33.3	182	2	C71839	phenylacrylic acid	805	4	33.3	194	2	S76919	nitroreductase fam
733	4	33.3	182	2	E69401	transcription anti	806	4	33.3	194	2	D87256	probable guanylate
734	4	33.3	182	2	S38870	transcription anti	807	4	33.3	195	2	D95946	probable NAD(P)H d
735	4	33.3	182	2	A89821	polypeptide (clone	808	4	33.3	195	2	D64829	early light-induce
736	4	33.3	182	2	PQ0252	hypothetical prote	809	4	33.3	196	2	S01056	hypothetical prote
737	4	33.3	182	2	B84387	starvation induced	810	4	33.3	196	2	T21347	chemotaxis protein
738	4	33.3	182	2	H84394	hypothetical prote	811	4	33.3	196	2	F64231	hypothetical prote
739	4	33.3	182	2	B90060	transcription anti	812	4	33.3	196	2	C84313	two-component resp
740	4	33.3	183	2	B98099	tetrahydromethanop	813	4	33.3	196	2	A12085	hypothetical prote
741	4	33.3	183	2	A69008	hypothetical prote	814	4	33.3	196	2	T10413	skp protein - Haem
742	4	33.3	183	2	T18193	hypothetical prote	815	4	33.3	197	2	E64102	conserved hypothet
743	4	33.3	183	2	T17492	hypothetical prote	816	4	33.3	197	2	AB3081	conserved hypothet
744	4	33.3	183	2	A45975	hypothetical prote	817	4	33.3	198	2	C69296	protein gp51 [Bact
745	4	33.3	183	2	A62498	nitr reductase	818	4	33.3	198	2	AC1364	hypothetical prote
746	4	33.3	184	2	B51131	nitr reductase	819	4	33.3	198	2	S77091	chorion protein S1
747	4	33.3	184	2	B91156	conserved hypothet	820	4	33.3	198	2	C32998	dCTP deaminase [im
748	4	33.3	184	2	G86001	conserved hypothet	821	4	33.3	199	2	AB1815	hypothetical 21.7k
749	4	33.3	184	2	G72309	conserved hypothet	822	4	33.3	199	2	G98205	urease accessory p
750	4	33.3	184	2	S65817	conserved hypothet	823	4	33.3	199	2	G98205	urease accessory p
751	4	33.3	185	1	B69374	dUDP-4-dehydroram	824	4	33.3	199	2	C71979	hypothetical prote
752	4	33.3	185	2	B69106	fkbp-type peptidyl	825	4	33.3	199	2	D64528	hypothetical luxR-
753	4	33.3	185	2	D71854	hypothetical prote	826	4	33.3	199	2	H70709	transcription init
754	4	33.3	186	2	B83727	hydrolase [impor	827	4	33.3	200	2	AG0986	probable outer mem
755	4	33.3	186	2	A12608	conserved hypothet	828	4	33.3	200	2	S21140	hypothetical prote
756	4	33.3	187	1	G69056	peptidyl-prolyl ci	829	4	33.3	200	2	B64653	probable bacteriop
757	4	33.3	187	2	G83243	bone morphogenetic	830	4	33.3	200	2	T30472	protein T1N15.21 [
758	4	33.3	187	2	PN0496	Probable 2-oxoglut	831	4	33.3	200	2	AB0620	
759	4	33.3	187	2	H64366		832	4	33.3	200	2	E96525	

833	4	33.3	200	2	F69047	hypothetical prote	906	4	33.3	210	2	T49858	hypothetical prote
834	4	33.3	200	2	AF2480	hypothetical prote	907	4	33.3	210	2	T36893	hypothetical prote
835	4	33.3	201	2	JC5476	junction-specific	908	4	33.3	210	2	AH1451	NADH oxidase homol
836	4	33.3	201	2	C75417	Holliday junction	909	4	33.3	211	1	CYRTB3	beta-crystallin B3
837	4	33.3	201	2	S77195	hypothetical prote	910	4	33.3	211	2	A84006	GTP pyrophosphokin
838	4	33.3	201	2	F98316	DNA-3-methyladenin	911	4	33.3	211	2	S77540	hypothetical prote
839	4	33.3	201	2	T41883	ACNPPV orf146 - Bo	912	4	33.3	211	2	E70253	hypothetical prote
840	4	33.3	201	2	D72868	ACNPPV orf146 - Bo	913	4	33.3	212	1	Q8BEC4	HQLF3 protein - hu
841	4	33.3	201	2	F83441	hypothetical prote	914	4	33.3	212	2	AD2356	AhpC/TSA family pr
842	4	33.3	201	2	C95271	probable RpoB6 RNA	915	4	33.3	212	2	E75334	ribonuclease HII -
843	4	33.3	202	2	I48195	CD3 epsilon - dog	916	4	33.3	212	2	A4994	eggshell protein 1
844	4	33.3	202	2	T29206	hypothetical prote	917	4	33.3	212	2	S48952	hypothetical prote
845	4	33.3	202	2	C90034	hypothetical prote	918	4	33.3	212	2	F64236	aryl hydrocarbon r
846	4	33.3	202	2	S72342	D-alanine-D-alanin	919	4	33.3	212	2	I50543	hypothetical prote
847	4	33.3	202	2	T36138	hypothetical prote	920	4	33.3	212	2	B83543	hypothetical prote
848	4	33.3	202	2	F69012	conserved hypotet	921	4	33.3	212	2	A97219	amine oxidase (fla
849	4	33.3	202	2	T10547	hypothetical prote	922	4	33.3	212	2	B28935	hypothetical prote
850	4	33.3	202	1	S45869	glutaredoxin homol	923	4	33.3	212	2	F72579	probable transcrip
851	4	33.3	203	1	BWECRV	ruvA protein - Esc	924	4	33.3	213	2	E64690	response regulator
852	4	33.3	203	2	C90950	Holliday junction	925	4	33.3	213	2	F71804	hypothetical prote
853	4	33.3	203	2	G85798	Holliday junction	926	4	33.3	213	2	S27625	hypothetical prote
854	4	33.3	203	2	AC0743	Holliday junction	927	4	33.3	213	2	E43256	mobilization prote
855	4	33.3	203	2	H64426	hypothetical prote	928	4	33.3	213	2	F87689	conserved hypotet
856	4	33.3	203	2	T45907	hypothetical prote	929	4	33.3	213	2	S07573	amine oxidase (fla
857	4	33.3	203	2	H90132	hypothetical prote	930	4	33.3	213	2	AD2412	hypothetical prote
858	4	33.3	204	2	D97231	o-Acetyltransferas	931	4	33.3	214	1	RGBSCA	regulatory protein
859	4	33.3	204	2	B90255	ABC transporter, A	932	4	33.3	214	2	T37237	H+-transporting AT
860	4	33.3	204	2	G82149	Holliday junction	933	4	33.3	214	2	H84131	hypothetical prote
861	4	33.3	204	2	AT0250	Holliday junction	934	4	33.3	214	2	A87276	hypothetical prote
862	4	33.3	204	2	G83034	urease accessory p	935	4	33.3	215	2	J50753	multicatalytic end
863	4	33.3	204	2	T41853	ACNPPV orf115 - Bo	936	4	33.3	215	2	A1261	peptidylprolyl iso
864	4	33.3	204	2	T47864	hypothetical prote	937	4	33.3	215	2	T03386	transcription init
865	4	33.3	204	2	E86836	hypothetical prote	938	4	33.3	215	2	C95352	hypothetical prote
866	4	33.3	204	2	F83067	hypothetical prote	939	4	33.3	215	2	C81731	hypothetical prote
867	4	33.3	205	2	G75535	deoxyguanosine kin	940	4	33.3	216	2	G97953	thymidine kinase (
868	4	33.3	205	2	A71177	probable thymidyla	941	4	33.3	216	2	T35881	uracil phosphoribo
869	4	33.3	205	2	C81665	Conserved hypotet	942	4	33.3	216	2	T40268	ubiquinone biosynt
870	4	33.3	205	2	AG0477	hemophore Hasa [im	943	4	33.3	216	2	S34205	coat protein homol
871	4	33.3	205	2	E90094	26S proteasome SU	944	4	33.3	216	2	S27899	hypothetical prote
872	4	33.3	205	2	H85072	hypothetical prote	945	4	33.3	216	2	S28714	hypothetical prote
873	4	33.3	206	1	TVHUAB	transforming prote	946	4	33.3	217	1	I67685	nitroreductase (EC
874	4	33.3	206	2	JN0623	GTP-binding protei	947	4	33.3	217	1	S08397	chloramphenicol O-
875	4	33.3	206	2	E71452	hypothetical prote	948	4	33.3	217	1	A24651	oxygen-insensitive
876	4	33.3	206	2	E82233	hypothetical prote	949	4	33.3	217	2	H90705	oxygen-insensitive
877	4	33.3	206	2	AF0269	conserved hypotet	950	4	33.3	217	2	C85556	glutathione transf
878	4	33.3	206	2	AO6553	conserved hypotet	951	4	33.3	217	2	AD0573	thiamin-phosphate
879	4	33.3	206	2	S50913	conserved hypotet	952	4	33.3	217	2	G69092	alpha fucosidase p
880	4	33.3	206	2	JC2070	TAF25 protein - ye	953	4	33.3	217	2	F64874	trypsin inhibitor
881	4	33.3	206	2	T25384	hypothetical prote	954	4	33.3	217	2	G71889	resolvase homolog
882	4	33.3	206	2	S68597	NADPH dehydrogenas	955	4	33.3	217	2	S65830	conserved hypotet
883	4	33.3	206	2	AF77943	NADPH dehydrogenas	956	4	33.3	217	2	S49578	probable translati
884	4	33.3	207	1	I64168	hypothetical prote	957	4	33.3	217	2	G69890	host range factor
885	4	33.3	207	1	B44994	probable translati	958	4	33.3	217	2	G69092	probable inorganic
886	4	33.3	207	2	C70855	eggshell protein 2	959	4	33.3	218	2	F64874	hypothetical colle
887	4	33.3	207	2	F98283	hypothetical prote	960	4	33.3	218	2	G90858	multiple sugar-bin
888	4	33.3	207	2	F98283	hypothetical prote	961	4	33.3	218	2	H85760	hypothetical prote
889	4	33.3	207	2	C70029	NADH dehydrogenase	962	4	33.3	218	2	T30415	hypothetical prote
890	4	33.3	207	2	T11900	multicatalytic end	963	4	33.3	218	2	H84561	Gnp-binding protel
891	4	33.3	208	2	S21126	hypothetical prote	964	4	33.3	218	2	T50324	response regulator
892	4	33.3	208	2	T05859	hypothetical prote	965	4	33.3	218	2	AG3554	avrPmaAI protein -
893	4	33.3	208	2	AD3353	probable glutathio	966	4	33.3	219	2	E75219	avrPpIAI protein -
894	4	33.3	208	2	F95892	hypothetical prote	967	4	33.3	219	2	G95372	hypothetical prote
895	4	33.3	208	2	AB2441	cytochrome o ubiq	968	4	33.3	220	2	JH0425	methyl-accepting c
896	4	33.3	209	2	AC2830	pyrazinamidase/nic	969	4	33.3	220	2	F72415	hypothetical prote
897	4	33.3	209	2	F83480	uracil phosphoribo	970	4	33.3	220	2	JQ1986	Gnp-binding protel
898	4	33.3	209	2	T19847	hypothetical prote	971	4	33.3	220	2	JQ1986	response regulator
899	4	33.3	209	2	AB1444	gp51 (Bacteriophag	972	4	33.3	220	2	T49575	avrPpIAI protein -
900	4	33.3	209	2	C82656	hypothetical prote	973	4	33.3	220	2	T49575	hypothetical prote
901	4	33.3	209	2	D97056	competence ComEa p	974	4	33.3	220	2	T72205	methyl-accepting c
902	4	33.3	210	2	T21898	hypothetical prote	975	4	33.3	220	2	T20880	hypothetical prote
903	4	33.3	210	2	H75215	conserved hypotet	976	4	33.3	221	2	AG3484	arylesterase precu
904	4	33.3	210	2	D84273	fibrillarlin [impor	977	4	33.3	221	2	A81329	probable two-compo
905	4	33.3	210	2	H81360	probable periplasm	978	4	33.3	221	2	S77396	hypothetical prote
													hypothetical prote

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979 4 33.3 221 2 AI0089 probable flagellar
980 4 33.3 222 2 T47768 hypothetical prote
981 4 33.3 222 2 G70484 cytidylate kinase
982 4 33.3 222 2 A88102 protein W09G10.1 [
983 4 33.3 223 2 D83314 probable two-compo
984 4 33.3 223 2 D72004 hypothetical prote
985 4 33.3 223 2 E86620 hypothetical prote
986 4 33.3 223 2 A91083 hypothetical prote
987 4 33.3 223 2 T30440 hypothetical prote
988 4 33.3 223 2 E65059 ABC transporter (A
989 4 33.3 223 2 D83869 hypothetical prote
990 4 33.3 223 2 C85928 thyrotropin-releas
991 4 33.3 224 2 S20382 hemoglobin linker
992 4 33.3 224 2 A35012 conserved hypothet
993 4 33.3 224 2 G69150 phosphoglycolate p
994 4 33.3 224 2 C97452 hydrolase [importe
995 4 33.3 224 2 AE2670 ribulose-phosphate
996 4 33.3 225 2 H90019 hypothetical prote
997 4 33.3 225 2 H97607 urease accessory p
998 4 33.3 225 2 E64075 glutathione transf
999 4 33.3 225 2 S33308 conserved hypothet
1000 4 33.3 225 2 D83200

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0512
R:Shimogashi, Y.; Matsumoto, H.; Takano, H.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragme
A:Reference number: PN0512; MUID:93290653
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SHI>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 12; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.7e-07; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12
| | | | | | | | | | | | | |
DB 1 DAEFRHDSGYEV 12
| | | | | | | | | | | | | |
RESULT 2
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
C:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 12; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
| | | | | | | | | | | | | |
DB 6 DAEFRHDSGYEV 17
| | | | | | | | | | | | | |
RESULT 3
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
C:Cross-references: EMBL:X56127; NID:gl895; PIDN:CAA39592.1; PID:gl896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 12; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.5e-07; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12
| | | | | | | | | | | | | |
DB 6 DAEFRHDSGYEV 17
| | | | | | | | | | | | | |
RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
C:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 12; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.5e-07; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12
| | | | | | | | | | | | | |
DB 6 DAEFRHDSGYEV 17
| | | | | | | | | | | | | |
RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56124

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 12; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

|||||

Db 6 DAEFRHDSGYEV 17

RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C;Accession: A60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079

A;Accession: A60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56125

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 12; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

|||||

Db 6 DAEFRHDSGYEV 17

RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C;Accession: B60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079

A;Accession: B60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 12; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

|||||

Db 6 DAEFRHDSGYEV 17

RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 186, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A;Reference number: PQ0438; MUID:93075180

A;Accession: PQ0438

A;Molecule type: DNA

A;Residues: 1-82 <DAV>

A;Cross-references: GB:M83558; GB:M83657

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A;Reference number: A60045; MUID:92017079

A;Accession: C60045

A;Molecule type: mRNA

A;Residues: 12-68 <JOH>

A;Cross-references: EMBL:X56129

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 12; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

|||||

Db 17 DAEFRHDSGYEV 28

RESULT 9

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A49795

R;Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A;Title: Homology of the amyloid beta protein precursor in monkey and human supports

A;Reference number: A49795; MUID:91273117

A;Accession: A49795

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-695 <POD>

A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C;Keywords: alternative splicing

Query Match 100.0%; Score 12; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

|||||

Db 597 DAEFRHDSGYEV 608

RESULT 10

QRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XfA inh

N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu

protein precursor splice form APP(770)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562;

4668; A28583; A29302; A60805; JLO038; S06121; A60355; A59011; A38384; S29076; S38252;

R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A;Title: The PrA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode

A;Reference number: S02260; MUID:89128427

Fri Sep 13 09:18:12 2002

A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
 A:Note: alternative splice form APP(695)
 R:La Fauri, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-protein
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity
 A:Reference number: A33260; MUID:89392050
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: DNA
 A:Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA

A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
 A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
 A:Experimental source: familial Alzheimer disease family LIT
 A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAM>
 A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A:Experimental source: brain
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TANI>
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
 EMO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'V', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;

Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor
A:Reference number: S00925; MUID:88122639
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X05989; EMBL:Y00297; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g9929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:88124954
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 559 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.
Query Match 100.0%; Score 12; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
|||||
Db 672 DAEFRHDSGYEV 683
RESULT 11
fatty aldehyde dehydrogenase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-Aug-2001
C:Accession: G87594
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87594
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-528 <STO>
A:Cross-references: GB:AE005673; NID:g13424391; PIDN:AAK24755.1; GSPDB:GN00148

C:Genetics:
A:Gene: CC2791
C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
Query Match 58.3%; Score 7; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 HDSGYEV 12
Db 219 HDSGYEV 225
RESULT 12
S54715
probable aspartate transaminase (EC 2.6.1.1) - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 23-Aug-1995 #sequence_revision 12-Dec-1997 #text_change 13-Sep-1998
C:Accession: S54715
R:Puttkhant, C.; Nihira, T.; Yamada, Y.
Mol. Gen. Genet. 247, 118-122, 1995
A:Title: Cloning, nucleotide sequence, and transcriptional analysis of the nusG gene
A:Reference number: S54715; MUID:95231511
A:Accession: S54715
A:Molecule type: DNA
A:Residues: 1-122 <PUT>
A:Cross-references: EMBL:D32254
A:Experimental source: strain A3(2), substrain SC
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase
Query Match 50.0%; Score 6; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 DSGYEV 12
Db 93 DSGYEV 98
RESULT 13
AG1140
transcription regulator (TipA from Streptomyces coelicolor) homolog lmo0526 [imported
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AG1140
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1140
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC98605.1; PID:g16409902; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0526
C:Superfamily: tipA protein
Query Match 50.0%; Score 6; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRH 6
|||||

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M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: G84709
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-447 <STO>
 A:Cross-references: GB:AE002093; NID:gl946364; PIDN:AAB63082.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g30550
 A:Map position: 2

Db 164 DAEFRH 169

RESULT 14

G69277
 branched-chain amino acid ABC transporter, periplasmic binding protein (brac-1) homolog C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: G69277
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Pyrococcus furiosus.
 A:Reference number: A69250; MUID:98049343
 A:Accession: G69277
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-380 <KLE>
 A:Cross-references: GB:AE001090; GB:AE000782; NID:g2689413; PIDN:AAB91009.1; PID:g265041

Query Match 50.0%; Score 6; DB 2; Length 380;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12

Db 131 DSGYEV 136

RESULT 15

T11786
 aspartate transaminase (EC 2.6.1.1) - Streptomyces virginiae
 N:Alternate names: aspartate aminotransferase
 C:Species: Streptomyces virginiae
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
 C:Accession: T11786
 R:Yamada, Y.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: Z17345
 A:Accession: T11786
 A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-397 <YAM>

A:Cross-references: EMBL:D50624

C:Genetics:

A:Gene: aat

A:Function:

A:Description: catalyzes the reversible transfer of the amino group from L-aspartate to

A:Pathway: aspartate catabolism

C:Superfamily: aspartate transaminase

C:Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate

Query Match

50.0%; Score 6; DB 2; Length 397;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12

Db 82 DSGYEV 87

RESULT 16

G84709
 probable lipase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84709
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

Query Match 50.0%; Score 6; DB 2; Length 447;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12

Db 88 DSGYEV 93

RESULT 17

C69543
 hypothetical protein AF2347 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: C69543
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343

A:Accession: C69543

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-453 <KLE>

A:Cross-references: GB:AE001114; GB:AE000782; NID:g2689437; PIDN:AAB91316.1; PID:g265

Query Match 50.0%; Score 6; DB 2; Length 453;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12

Db 107 DSGYEV 112

RESULT 18

H86202
 hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: H86202

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: H86202

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-515 <STO>
A:Cross-references: GB:AE005172; NID:g7523699; PIDN:AAF63138.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 50.0%; Score 6; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
|||||
Db 154 DSGYEV 159

RESULT 19
TI5776
hypothetical protein C34F11.9a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: TI5776

R:Bentley, D.
submitted to the EMBL Data Library, January 1996
A:Description: The sequence of C. elegans cosmid C34F11.
A:Reference number: Z18400
A:Accession: TI5776

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-761 <BEN>
A:Cross-references: EMBL:U46753; NID:g1166623; PID:g1166632; PIDN:AAA85766.1; CESP:C34F11
C:Genetics:
A:Gene: CESP:C34F11.9a
A:Introns: 41/1; 73/3; 123/2; 196/1; 228/1; 413/1; 438/2; 479/1; 559/2; 618/1; 693/1

Query Match 50.0%; Score 6; DB 2; Length 761;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
|||||
Db 120 DSGYEV 125

RESULT 20
AE1915
hypothetical protein all0872 [imported] - Anabaena sp. (strain PCC 7120)
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AE1915
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. (strain PCC 7120)
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1915

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1237 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072829.1; PID:g17130217; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0872

Query Match 50.0%; Score 6; DB 2; Length 1237;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRH 6
|||||

Db 424 DAEFRH 429

RESULT 21

AB2042
hypothetical protein all1888 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AB2042
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. (strain PCC 7120)
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2042

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1256 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073587.1; PID:g17130978; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1888

Query Match 50.0%; Score 6; DB 2; Length 1256;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRH 6
|||||
Db 441 DAEFRH 446

RESULT 22

AB6604
periplasmic divalent cation tolerance protein [imported] - Chlamydia pneumoniae (strain PCC 7120)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: AB6604
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: AB6491; MUID:20330349
A:Accession: AB6604

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <STO>
A:Cross-references: GB:BA000008; NID:g8979281; PIDN:BAA99115.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: cutA
C:Superfamily: divalent cation tolerance protein cutA1

Query Match 41.7%; Score 5; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
|||||
Db 76 SGYEV 80

RESULT 23

B72019
periplasmic divalent cation tolerance protein CutA1 Cp0959 [imported] - Chlamydia pneumoniae (strain PCC 7120)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
C:Accession: B72019; F81520
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

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A:Reference number: A72000; MUID:99206606
A:Accession: B72019
A:Molecule type: DNA
A:Residues: 1-112 <ARN>
A:Cross-references: GB:AE001671; GB:AE001363; NID:g4377226; PIDN:AAD19045.1; PID:g437722
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255
A:Accession: F81520
A:Molecule type: DNA
A:Residues: 1-112 <REA>
A:Cross-references: GB:AE002253; GB:AE002161; NID:g7189859; PIDN:AAF38739.1; PID:g718987
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: cutA; CP0959
C:Superfamily: divalent cation tolerance protein cutA1

Query Match 41.7%; Score 5; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY 8 SGYEV 12
Db 76 SGYEV 80

RESULT 24
G90310
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: G90310
R:Sheng, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90310
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <KUR>
A:Cross-references: GB:AE006641; NID:g13814752; PIDN:AAK41742.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1520

Query Match 41.7%; Score 5; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY 7 DSGYE 11
Db 73 DSGYE 77

RESULT 25
H72479
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339
A:Accession: H72479
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-123 <KAW>
A:Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAAR81496.1; PID:d1045282; PID:g
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2480

Query Match 41.7%; Score 5; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY 8 SGYEV 12
Db 65 SGYEV 69

RESULT 26
S68170
N:Alternate names: anti-cytomegalovirus glycoprotein B antibody
C:Species: Homo sapiens (man)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C:Accession: S68170
R:Boeldicke, T.; Haase, B.; Boecher, M.; Lindenmaier, W.
Eur. J. Biochem. 234, 397-405, 1995
A:Title: Human monoclonal antibodies to cytomegalovirus. Characterization and recombi
A:Reference number: S68170; MUID:96128166
A:Accession: S68170
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-125 <BOE>
A:Cross-references: GB:S80750; NID:gl246061; PIDN:AAB35861.1; PID:gl246062
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 5; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY 8 SGYEV 12
Db 105 SGYEV 109

RESULT 27
JQ0737
R:RpA protein - Micrococcus luteus
C:Species: Micrococcus luteus, Micrococcus lysodeikticus
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 15-Oct-1999
C:Accession: JQ0737
R:Fujita, M.Q.; Yoshikawa, H.; Ogasawara, N.
Gene 93, 73-78, 1990
A:Title: Structure of the dnaA region of Micrococcus luteus: conservation and variati
A:Reference number: JQ0737; MUID:91033019
A:Accession: JQ0737
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <FUJ>
A:Cross-references: GB:M34006; NID:gl49845; PIDN:AAA25313.1; PID:g455290
C:Superfamily: Streptomyces ribonuclease P, protein component

Query Match 41.7%; Score 5; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY 2 AEFRR 6
Db 12 AEFRR 16

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RESULT 28
R3TW12
ribosomal protein S12 - Thermus aquaticus
C:Species: Thermus aquaticus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21-Jan-2000
C:Accession: S10249; S51053; F48401
R:Yakhnin, A.V.; Vorozheynkina, D.P.; Matvienko, N.I.
Nucleic Acids Res. 18, 3659, 1990
A:Title: Nucleotide sequence of the Thermus thermophilus HB8 rps12 and rps7 genes coding
A:Reference number: S10249; MUID:90301504
A:Accession: S10249
A:Molecule type: DNA
A:Residues: 1-135 <YAK>
A:Cross-references: EMBL:X52165; NID:q48273; PIDN:CAA36418.1; PID:g581812
A:Experimental source: strain HB8
A>Note: the source is designated as Thermus thermophilus
R:Tsolli, P.; Herfurth, E.; Choli, T.
Eur. J. Biochem. 226, 169-177, 1994
A:Title: Purification and characterization of the 30S ribosomal proteins from the bacter
A:Reference number: S51053; MUID:95045586
A:Accession: S51053
A:Molecule type: protein
A:Residues: 5-32 <TSI>
A>Note: the source is given as Thermus thermophilus
R:Garber, M.B.; Agalarov, S.C.; Eliseikina, I.A.; Fomenkova, N.P.; Nikonov, S.V.; Sedeln
Biochimie 74, 327-336, 1992
A:Title: Ribosomal proteins from Thermus thermophilus for structural investigations.
A:Reference number: A48401; MUID:92345325
A:Accession: F48401
A:Molecule type: protein
A:Residues: V, 6-11 <GAR>
A>Note: the source is given as Thermus thermophilus
C:Genetics:
A:Start codon: GTG
C:Superfamily: Escherichia coli ribosomal protein S12
C:Keywords: protein biosynthesis; ribosome
F:5-135/Product: ribosomal protein S12 #status predicted <MAT>
F:92/Modified site: beta-methylthioaspartic acid (Asp) #status predicted

Query Match 41.7%; Score 5; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
Db 62 SGYEV 66

RESULT 29
A34653
cell adhesion protein SQM1 - human
C:Species: Homo sapiens (man)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 21-Jul-2000
C:Accession: A34653
R:Wong, Y.C.; Tsao, S.W.; Kakefuda, M.; Bernal, S.D.
Biochem. Biophys. Res. Commun. 166, 984-992, 1990
A:Title: cDNA Cloning of a novel cell adhesion protein expressed in human squamous carci
A:Reference number: A34653; MUID:90147818
A:Accession: A34653
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <WON>
A:Cross-references: GB:M33374; NID:g180232; PIDN:AAA35675.1; PID:g180233
C:Keywords: cell adhesion

Query Match 41.7%; Score 5; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHDSG 9

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Db 83 RHDSG 87

RESULT 30
A87681
conserved hypothetical protein CC3483 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: A87681
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87681
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <STO>
A:Cross-references: GB:AE005673; NID:g13425207; PIDN:AAK25445.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3483

Query Match 41.7%; Score 5; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRR 6
Db 30 AEFRR 34

RESULT 31
E89026
protein F13A2.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: E89026
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/c_elegans/ and www.sanger.ac.uk/projects/C-
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: E89026
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <STO>
A:Cross-references: GB:chr_V; PIDN:AAB69895.1; PID:g2384795; GSPDB:GN00023; CESP:F13A
C:Genetics:
A:Gene: F13A2.1
A:Map position: 5

Query Match 41.7%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 60 DAEFR 64

RESULT 32
E90265
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: E90265
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder

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arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: E90265
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143 <KUR>
A:Cross-references: GB:AE006641; NID:gl13814314; PIDN:AAK41380.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS01126

Query Match          41.7%; Score 5; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 SGYEV 12
    |||||
Db  34 SGYEV 38

RESULT 33
S62510
hypothetical protein SPAC30.08 [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 18-Aug-2000
C:Accession: S62510; T38505; T50214
R:Jones, L.; Murphy, L.; McNeil, A.; Simpson, I.; Harris, D.
submitted to the EMBL Data Library, October 1995
A:Reference number: S62507
A:Accession: S62510
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <JON>
A:Cross-references: EMBL:Z66525; NID:gl044926; PIDN:CAA91426.1; PID:gl044930
R:Jones, L.; Murphy, L.; McNeil, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, October 1995
A:Reference number: T38505
A:Accession: T38505
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-145 <JO2>
A:Cross-references: EMBL:Z66525; PIDN:CAA91426.1; GSPDB:GN00066; SPDB:SPAC29E6.04
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; M
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25046
A:Accession: T50214
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <MCD>
A:Cross-references: EMBL:AL136538; PIDN:CAB66467.1; GSPDB:GN00066; SPDB:SPAC30.08
A:Experimental source: strain 972h(-); cosmid c29E6
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; M
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25046
A:Accession: T50214
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <MCD>
A:Cross-references: EMBL:AL136538; PIDN:CAB66467.1; GSPDB:GN00066; SPDB:SPAC30.08
A:Experimental source: strain 972h(-); cosmid c30
C:Genetics:
A:Gene: SPAC29E6.04; SPAC30.08
A:Map position: 1
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC30.08

Query Match          41.7%; Score 5; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DAEFR 5
    |||||
Db  82 DAEFR 86

RESULT 34
S30698
cyax protein - Escherichia coli
N:Alternate names: hypothetical 17.3k protein (cyax region)
C:Species: Escherichia coli
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 08-Oct-1999
C:Accession: S30698; A30264; A65185
R:Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.
Science 257, 771-778, 1992
A:Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.
A:Reference number: S30660; MUID:92358234
A:Accession: S30698
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-161 <DAN>
A:Cross-references: EMBL:M87049; NID:g836656; PIDN:AAA67604.1; PID:gl48207
R:Alba, H.; Mori, K.; Tanaka, M.; Ooi, T.; Roy, A.; Danchin, A.
Nucleic Acids Res. 12, 9427-9440, 1984
A:Title: The complete nucleotide sequence of the adenylate cyclase gene of Escherich
A:Reference number: A93552; MUID:85087947
A:Accession: A30264
A:Molecule type: DNA
A:Residues: 1-116 <AIB>
A:Cross-references: GB:X01653; GB:J01599; GB:K02969; GB:M68875; GB:V00271; NID:g41182
A:Note: cyax gene located downstream from cya seems to specify a very hydrophobic pro
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: A65185
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-161 <BLAT>
A:Cross-references: GB:AE000456; GB:U00096; NID:g2367291; PIDN:ARC76811.1; PID:gl7902
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: cyax
A:Map position: 85 min
C:Superfamily: Escherichia coli cyax protein

Query Match          41.7%; Score 5; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 FRHDS 8
    |||||
Db  98 FRHDS 102

RESULT 35
T34963
hypothetical protein SC4A10.26 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000
C:Accession: T34963
R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21563
A:Accession: T34963
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-167 <SAU>
A:Cross-references: EMBL:AL109663; PIDN:CAB52002.1; GSPDB:GN00070; SC0EDB:SC4A10.26
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SC0EDB:SC4A10.26
C:Superfamily: Methanobacterium thermoautotrophicum carbonic anhydrase

Query Match          41.7%; Score 5; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 EFRHD 7

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Db 103 EFRHD 107

RESULT 36
T31347
hypothetical protein G01D9.3 - Caenorhabditis briggsae
C:Species: Caenorhabditis briggsae
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31347
R:Waterston, R.
submitted to the EMBL Data Library, April 1996
A:Description: The C. briggsae genome sequencing project.
A:Reference number: Z21010
A:Accession: T31347
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-186 <WAT>
A:Cross-references: EMBL:U56248; NID:g1293789; PID:g1293792; PIDN:AAA98701.1
C:Genetics:
A:Introns: 51/2; 101/3; 141/3
A:Note: G01D9.3

Query Match 41.7%; Score 5; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 47 DAEFR 51

RESULT 37
B70577
hypothetical protein RV2134c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70577
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: B70577
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-195 <COL>
A:Cross-references: GB:295388; GB:ALL23456; NID:g3261759; PIDN:CAB08659.1; PID:g2104344
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV2134c

Query Match 41.7%; Score 5; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 87 DAEFR 91

RESULT 38
S72861
hypothetical protein B2136_C3_228 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C:Accession: S72861
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993

A:Description: Mycobacterium leprae cosmid B2126.
A:Reference number: S72585
A:Accession: S72861
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <SMI>
A:Cross-references: EMBL:U00017; NID:g466994; PIDN:AAAL7201.1; PID:g467016

Query Match 41.7%; Score 5; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 87 DAEFR 91

RESULT 39
T21689
hypothetical protein F33A8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T21689
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19459
A:Accession: T21689
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <WIL>
A:Cross-references: EMBL:Z81525; PIDN:CAB04257.1; GSPDB:GN00020; CESP:F33A8.3
A:Experimental source: clone F33A8
C:Genetics:
A:Gene: CESP:F33A8.3
A:Map position: 2
A:Introns: 5/3; 174/3
C:Superfamily: Arabidopsis glycine-rich protein 2; cold shock domain homology
F:23-87/Domain: cold shock domain homology <CSD>

Query Match 41.7%; Score 5; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHD5G 9
Db 128 RHD5G 132

RESULT 40
T35041
hypothetical protein SC4G2.06 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 04-Mar-2000
C:Accession: T35041
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21566
A:Accession: T35041
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-209 <SEE>
A:Cross-references: EMBL:AL031371; PIDN:CAA20543.1; GSPDB:GN00070; SCOEDB:SC4G2.06
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC4G2.06
C:Superfamily: Streptomyces coelicolor hypothetical protein SC4G2.06

Query Match 41.7%; Score 5; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba Nature 405, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals
 A:Reference number: A81250; MUID:20150912
 A:Accession: B81362
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 <PAR>
 A:Cross-references: GB:ALJ39076; GB:ALJ11168; NID:g6968128; PIDN:CA873148.1; PID:g696
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj0890c
 C:Superfamily: ompR protein; response regulator homology

Query Match 41.7%; Score 5; DB 2; Length 220;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 SGYEV 12
 Db 26 SGYEV 30
 |||||
 |||||

RESULT 44
 D83875
 hypothetical protein BH1804 [imported] - *Bacillus halodurans* (strain C-125)
 C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: D83875
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: D83875
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-226 <STO>
 A:Cross-references: GB:AP001513; GB:BA000004; NID:gl0174345; PIDN:BA805523.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH1804

Query Match 41.7%; Score 5; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 SGYEV 12
 Db 154 SGYEV 158
 |||||
 |||||

RESULT 45
 A13304
 response regulator ctra [imported] - *Brucella melitensis* (strain 16M)
 C:Species: *Brucella melitensis*
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
 C:Accession: A13304
 R:Belvecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
 ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzei, P.H.; Hagius, S.; O'Callaghan, D.; Let
 proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*
 A:Reference number: AD3252; PMID:11756688
 A:Accession: A13304
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-232 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL51604.1; PID:gl79823239; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0423
 A:Map position: I

Query Match 41.7%; Score 5; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 RHDSS 9
 Db 51 RHDSS 55
 |||||
 |||||

RESULT 43
 B81362
 probable sensory transduction transcription regulator Cj0890c [imported] - *Campylobacter*
 C:Species: *Campylobacter jejuni*
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
 C:Accession: B81362
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin

QY 1 DAEFR 5
 |||||
 Db 142 DAEFR 146
 |||||
 |||||

RESULT 41
 VCWZMW
 coat protein - maize white line mosaic satellite virus
 C:Species: maize white line mosaic satellite virus
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
 C:Accession: A38543
 R:Zhang, L.; Zitter, T.A.; Palukaitis, P. Virology 180, 467-473, 1991
 A:Title: Helper virus-dependent replication, nucleotide sequence and genome organization
 A:Reference number: A38543; MUID:91111965
 A:Accession: A38543
 A:Molecule type: genomic RNA
 A:Residues: 1-218 <ZHA>
 A:Cross-references: EMBL:M5012; NID:g335126; PIDN:AAA47885.1; PID:g335127
 C:Comment: This virus has not been classified.
 C:Superfamily: satellite tobacco necrosis virus coat protein
 C:Keywords: coat protein

Query Match 41.7%; Score 5; DB 1; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 SGYEV 12
 Db 132 SGYEV 136
 |||||
 |||||

RESULT 42
 C84280
 ABC-type transport protein [imported] - *Halobacterium* sp. NRC-1
 C:Species: *Halobacterium* sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: C84280
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
 ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jahlb
 Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
 A:Title: Genome sequence of *Halobacterium* species NRC-1.
 A:Reference number: A84160; MUID:20504483
 A:Accession: C84280
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <STO>
 A:Cross-references: GB:AE004437; NID:gl0580775; PIDN:AAG19607.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: ybhF
 C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 41.7%; Score 5; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 RHDSS 9
 Db 51 RHDSS 55
 |||||
 |||||

RESULT 43
 B81362
 probable sensory transduction transcription regulator Cj0890c [imported] - *Campylobacter*
 C:Species: *Campylobacter jejuni*
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
 C:Accession: B81362
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin

C:Superfamily: ompR protein; response regulator homology

Query Match 41.7%; Score 5; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
|||||
Db 58 SGYEV 62

RESULT 46

A:Title: response regulator ctra (AF288464) [imported] - Agrobacterium tumefaciens (strain C58, C58)
C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C:Accession: A97652

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouellet, B.; Goldman, S.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A:Reference number: A97359; PMID:11743194

A:Accession: A97652

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK88170.1; PID:g15157614; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C_4416

A:Map position: circular chromosome

C:Superfamily: ompR protein; response regulator homology

Query Match 41.7%; Score 5; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
|||||
Db 58 SGYEV 62

RESULT 47

AH2875

C:Species: two component response regulator ctra [imported] - Agrobacterium tumefaciens (strain C58)
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C:Accession: AH2875

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, D.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.; E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AH2875

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <KUR>

A:Cross-references: GB:AE00688; PIDN:AAL43422.1; PID:g17740923; GSPDB:GN00186

C:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: ctra

A:Map position: circular chromosome

C:Superfamily: ompR protein; response regulator homology

Query Match 41.7%; Score 5; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
|||||
Db 58 SGYEV 62

RESULT 48

I38016

A:Title: melanoma-associated antigen CD63 [validated] - human
N:Alternates names: antigen ME491; lysosomal membrane glycoprotein CD63; ME491/CD63 an

C:Species: Homo sapiens (man)

C:Date: 17-May-1996 #sequence_revision 09-Aug-1996 #text_change 08-Dec-2000

C:Accession: I38016; S01418; A39514; B3826; A61177; A61173; A56782

R:Hotta, H.; Miyamoto, H.; Hara, I.; Takahashi, N.; Homma, M.

Biochem. Biophys. Res. Commun. 185, 436-442, 1992

A:Title: Genomic structure of the ME491/CD63 antigen gene and functional analysis of

A:Reference number: I38016; MUID:92287132

A:Accession: I38016

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-238 <RES>

A:Cross-references: EMBL:X62654; NID:g430755; PIDN:CAA44519.1; PID:g430756

R:Hotta, H.; Ross, A.H.; Huebner, K.; Isobe, M.; Wendeborn, S.; Chao, M.V.; Ricciardi

Cancer Res. 48, 2955-2962, 1988

A:Title: Molecular cloning and characterization of an antigen associated with early s

A:Reference number: S01418; MUID:88210273

A:Accession: S01418

A:Molecule type: mRNA

A:Residues: 1-238 <HOT>

A:Cross-references: EMBL:X07982; NID:g43526; PIDN:CAA30792.1; PID:g34527

R:Metzelaar, M.J.; Wijngaard, P.L.J.; Peters, P.J.; Sixma, J.J.; Nieuwenhuis, H.K.; C

J. Biol. Chem. 266, 3239-3245, 1991

A:Title: CD63 antigen. A novel lysosomal membrane glycoprotein, cloned by a screening

A:Reference number: A39514; MUID:91131632

A:Accession: A39514

A:Molecule type: mRNA

A:Residues: 1-238 <MET>

A:Cross-references: GB:M58485

R:Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wenpe, F.; Zimmer, M.; Scheit,

DNA Cell Biol. 9, 479-485, 1990

A:Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.

A:Reference number: A35826; MUID:91025550

A:Accession: B35826

A:Molecule type: mRNA

A:Residues: 1-238 <RAP>

A:Cross-references: GB:M59907; NID:g189383; PIDN:AAA63235.1; PID:g189384

R:Azorsa, D.O.; Hyman, J.A.; Hildreth, J.E.K.

Blood 78, 280-284, 1991

A:Title: CD63/Pitp40: a platelet activation antigen identical to the stage-specific,

A:Reference number: A61177; MUID:91300080

A:Accession: A61177

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 2-68, 'p', 70-238 <AZO>

R:Hildreth, J.E.K.; Derr, D.; Azorsa, D.O.

Blood 77, 121-132, 1991

A:Title: Characterization of a novel self-associating Mr 40,000 platelet glycoprotein

A:Reference number: A61173; MUID:91084576

A:Accession: A61173

A:Molecule type: protein

A:Residues: 2-8, 'X', 10-16, 'XX', 19-21 <HIL>

R:Wang, M.X.; Earley Jr., J.J.; Shields, J.A.; Donoso, L.A.

Arch. Ophthalmol. 110, 399-404, 1992

A:Title: An ocular melanoma-associated antigen. Molecular characterization.

A:Reference number: A56782; MUID:92181348

A:Accession: A56782

A:Molecule type: mRNA

A:Residues: 1-238 <WAN>

A:Cross-references: GB:S93788; NID:g246538; PIDN:AAB21617.1; PID:g246539

A:Experimental source: uveal melanoma

A:Note: sequence extracted from NCBI backbone (NCBIN:93788, NCBI:93790)

C:Genetics:

A:Gene: GDB:CD63; MLAI

Fri Sep 13 09:18:12 2002

A:Title: Molecular cloning of the murine homologue of CD63/ME491 and detection of its
A:Reference number: S43511; MUID:94198294

A:Accession: S43511
A:Molecule type: mRNA
A:Residues: 1-238 <MIY>
A:Cross-references: EMBL:D16432; NID:g484052; PIDN:BAA03904.1; PID:g976238
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F:1-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-51/Domain: extracellular #status predicted <EX1>
F:52-76/Domain: transmembrane #status predicted <TM2>
F:77-80/Domain: intracellular #status predicted <CY2>
F:81-103/Domain: transmembrane #status predicted <TM3>
F:104-202/Domain: extracellular #status predicted <EX2>
F:203-228/Domain: transmembrane #status predicted <TM4>
F:229-238/Domain: intracellular #status predicted <CY3>
F:116,130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.7%; Score 5; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
|||||
Db 233 SGYEV 237

Search completed: September 13, 2002, 09:06:36
Job time: 147 sec

A:Cross-references: GDB:I20186; OMIM:155740
A:Map position: 12q12-12q13
A:Introns: 22/3; 85/3; 110/3; 142/3; 189/3; 217/3
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F:2-238/Product: melanoma-associated antigen ME491 #status experimental <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-51/Domain: extracellular #status predicted <EX1>
F:52-76/Domain: transmembrane #status predicted <TM2>
F:77-80/Domain: intracellular #status predicted <CY2>
F:81-103/Domain: transmembrane #status predicted <TM3>
F:104-202/Domain: extracellular #status predicted <EX2>
F:203-228/Domain: transmembrane #status predicted <TM4>
F:229-238/Domain: intracellular #status predicted <CY3>
F:130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.7%; Score 5; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
|||||
Db 233 SGYEV 237

RESULT 49
JC2297
CD63 antigen - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 28-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C:Accession: JC2297
R:Shima, Y.; Suzuki, T.; Sasano, H.; Nagura, H.; Nose, M.; Yamamoto, T.
Cell Struct. Funct. 19, 219-225, 1994
A:Title: Increased mRNA for CD63 antigen in atherosclerotic lesions of Watanable heritable
A:Reference number: JC2297; MUID:95120837
A:Accession: JC2297
A:Molecule type: mRNA
A:Residues: 1-238 <SOH>
A:Cross-references: DDBJ:D21264; NID:g684973; PIDN:BAA04804.1; PID:g684974
A:Experimental source: aorta
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F:1-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-51/Domain: extracellular #status predicted <EX1>
F:52-76/Domain: transmembrane #status predicted <TM2>
F:77-80/Domain: intracellular #status predicted <CY2>
F:81-103/Domain: transmembrane #status predicted <TM3>
F:104-202/Domain: extracellular #status predicted <EX2>
F:203-228/Domain: transmembrane #status predicted <TM4>
F:229-238/Domain: intracellular #status predicted <CY3>
F:125,130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.7%; Score 5; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
|||||
Db 233 SGYEV 237

RESULT 50
S43511
CD63/ME491 antigen homolog - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C:Accession: S43511
R:Miyamoto, H.; Homma, M.; Hotta, H.
Biochim. Biophys. Acta 1217, 312-316, 1994

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:05:50 ; Search time 10.38 Seconds
(without alignments)
44.762 Million cell updates/sec

Title: US-09-580-015-42_COPY_1_12
Perfect score: 12
Sequence: 1 DAEFRHDSGVEV 12

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	12	100.0	57	1 A4_URSNA	Q29149 ursus marit
3	12	100.0	58	1 A4_CANFA	Q28280 canis famil
4	12	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	12	100.0	58	1 A4_SHEEP	Q28757 ovis aries
6	12	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	12	100.0	751	1 A4_SAYS	Q95241 salmieri sci
8	12	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	6	50.0	213	1 AAT_STRGR	P36692 streptomyce
10	6	50.0	397	1 AAT_STRVG	Q60013 streptomyce
11	5	41.7	90	1 EFIB_AERPE	Q94904 aeropyrum p
12	5	41.7	107	1 T2AH_DROME	Q945b9 drosophila
13	5	41.7	132	1 RNPA_MICLU	P21172 micrococcc
14	5	41.7	135	1 RS12_THERH	P17293 thermus aqu
15	5	41.7	145	1 YAF4_SCHPO	Q98588 schizosacch
16	5	41.7	150	1 RNK6_MIOFA	O46531 miopithecus
17	5	41.7	161	1 Y2CX_ECOLI	P11291 escherichia
18	5	41.7	218	1 COAT_SMWLM	P29151 satelllite m
19	5	41.7	236	1 CD63_BOVIN	Q98xk2 bos taurus
20	5	41.7	237	1 CD63_HUMAN	P08962 homo sapien
21	5	41.7	237	1 CD63_MOUSE	P41731 mus musculu
22	5	41.7	237	1 CD63_RABIT	Q28709 oryctolagus
23	5	41.7	237	1 CD63_RAT	P38648 rattus norv
24	5	41.7	258	1 FABI_SYNY3	P73016 synechocyst
25	5	41.7	269	1 T2S1_STRFI	O52512 streptomyce
26	5	41.7	285	1 PNMT_RAT	P10937 rattus norv
27	5	41.7	291	1 AMPM_CHLMU	Q9p168 chlamydia m
28	5	41.7	294	1 ATPB_MOUSE	P50992 mus musculu
29	5	41.7	310	1 PRFB_MOUSE	Q9cf79 lactococcc
30	5	41.7	314	1 IKBA_PIG	Q08353 sus scrofa
31	5	41.7	314	1 IKBA_RAT	Q63746 rattus norv
32	5	41.7	317	1 IKBA_HUMAN	P25963 homo sapien
33	5	41.7	318	1 IKBA_CHICK	Q91974 gallus gall

34	5	41.7	329	1	TECB_CHICK	P54097 gallus gall
35	5	41.7	331	1	GALR_LACCA	O84905 lactobacill
36	5	41.7	331	1	UL38_HCMVA	P16779 human cytom
37	5	41.7	336	1	Y724_METH	O26820 methanobact
38	5	41.7	340	1	ASTG_PSEAE	P80358 pseudomonas
39	5	41.7	343	1	TP38_TREPA	O56328 treponema p
40	5	41.7	382	1	MTLD_BACST	O45421 bacillus st
41	5	41.7	398	1	TAP_DROME	O16867 drosophila
42	5	41.7	399	1	PNCB_BUCAI	P57442 buchnera ap
43	5	41.7	399	1	PNCB_ECOLI	P18133 escherichia
44	5	41.7	399	1	PNCB_SALTY	P22253 salmonella
45	5	41.7	403	1	RSBP_BACSU	O07014 bacillus su
46	5	41.7	423	1	SUFD_ECOLI	P77689 escherichia
47	5	41.7	438	1	TRME_UREPA	O9prc7 ureaplasma
48	5	41.7	451	1	DPD2_CAEEL	O19366 caenorhabdi
49	5	41.7	465	1	SVC_HELPJ	O924w6 helicobacte
50	5	41.7	465	1	SVC_HELPY	P41359 helicobacte
51	5	41.7	483	1	SVC_SYNY3	P74330 synechocyst
52	5	41.7	489	1	YS45_CAEEL	Q09660 caenorhabdi
53	5	41.7	504	1	C6AL_DROME	O9v774 drosophila
54	5	41.7	519	1	ALAB_HUMAN	P35368 homo sapien
55	5	41.7	537	1	CYDA_AZOVI	O90949 azotobacter
56	5	41.7	539	1	PRR1_SCHPO	O14283 schizosacch
57	5	41.7	570	1	STIM_DROME	P83094 drosophila
58	5	41.7	574	1	5NTD_HUMAN	P21589 homo sapien
59	5	41.7	577	1	VGLE_PVRRI	P08354 pseudorabie
60	5	41.7	611	1	YD3M_HERAU	P25280 herpetosiph
61	5	41.7	632	1	ARPB_ECOLI	P76205 escherichia
62	5	41.7	632	1	FMN2_HUMAN	O9az56 homo sapien
63	5	41.7	644	1	C3AA_BACTT	P07130 bacillus th
64	5	41.7	647	1	YIK1_YEAST	P40489 saccharomyc
65	5	41.7	649	1	C3CA_BACTK	O45744 bacillus th
66	5	41.7	670	1	C2ID_HUMAN	O95447 homo sapien
67	5	41.7	693	1	LYS4_YEAST	P49367 saccharomyc
68	5	41.7	750	1	STAI_HUMAN	P42224 homo sapien
69	5	41.7	857	1	TOPI_SYNY3	O18381 drosophila
70	5	41.7	898	1	PAX6_DROME	P73810 synechocyst
71	5	41.7	900	1	GLND_PSEAE	Q929h0 pseudomonas
72	5	41.7	947	1	PMAA_ARATH	Q43128 arabidopsis
73	5	41.7	953	1	COPE_HUMAN	P53618 homo sapien
74	5	41.7	953	1	COPE_MOUSE	Q911f7 mus musculu
75	5	41.7	953	1	COPE_RAT	P23514 rattus norv
76	5	41.7	1295	1	GLP1_CAEEL	P13508 caenorhabdi
77	5	41.7	1567	1	FMN2_MOUSE	Q91104 mus musculu
78	5	41.7	1668	1	DPOL_THERY	Q9hh05 thermococcu
79	5	41.7	1840	1	SUIS_RAT	P27339 rattus norv
80	5	41.7	2127	1	RRPL_RABVS	P12123 rabies viru
81	5	41.7	2142	1	RRPL_RABVP	Q9wvc7 rattus norv
82	5	41.7	2314	1	AKA6_RAT	P81133 bos taurus
83	5	41.7	2871	1	FBN1_BOVIN	P98133 bos taurus
84	5	41.7	2871	1	FBN1_HUMAN	P35555 homo sapien
85	5	41.7	2871	1	FBN1_MOUSE	Q81554 mus musculu
86	5	41.7	2871	1	FBN1_PIG	Q9cv36 sus scrofa
87	4	33.3	15	1	MAOX_CHICK	Q92060 gallus gall
88	4	33.3	39	1	NPF_HELAS	P41321 helix asper
89	4	33.3	43	1	VG67_BPML5	O5281 mycobacteri
90	4	33.3	58	1	YF97_ARCFU	O28675 archaeoglob
91	4	33.3	59	1	SECE_TREPA	O83263 treponema p
92	4	33.3	61	1	TBA4_MAIZE	P33636 zea mays p
93	4	33.3	62	1	SCX1_TITBA	P56608 titius bahi
94	4	33.3	63	1	YF82_SYNP2	P32040 synechococc
95	4	33.3	65	1	VF08_VACCP	P29887 vaccinia vi
96	4	33.3	67	1	ATPE_SCHPO	P87316 schizosacch
97	4	33.3	72	1	YA94_ARCFU	O29171 archaeoglob
98	4	33.3	73	1	PHD_BpP1	Q06253 bacterioph
99	4	33.3	74	1	SC17_MESMA	Q9njc4 mesobuthus
100	4	33.3	75	1	Y14E_BP74	P39508 bacterioph
101	4	33.3	75	1	Y14E_BP76	Q38168 bacterioph
102	4	33.3	76	1	TX3B_AGBAP	P81744 agelenopsis
103	4	33.3	80	1	SCX1_TITSE	P01496 titius serr
104	4	33.3	80	1	SCX4_TITSE	P45659 titius serr
105	4	33.3	81	1	HEMP_YEREN	P31516 yersinia en
106	4	33.3	84	1	Y169_METH	O26271 methanobact

107	4	33.3	87	1	CNRG_HUMAN	P19545	homo sapien	180	4	33.3	161	1	LA52_LYCES	P13447	lycopersico
108	4	33.3	87	1	Y04A_BPT4	P07083	bacterioph	181	4	33.3	162	1	YB09_SCHPO	P87150	schizosacch
109	4	33.3	89	1	TATA_HAEN	P57046	haemophilus	182	4	33.3	162	1	Y127_MYCTU	Q50605	mycobacteri
110	4	33.3	89	1	Y916_METJA	Q58326	methanococc	183	4	33.3	164	1	Y0HA_ECOLI	P52082	escherichia
111	4	33.3	97	1	ABC2_BPP22	P11191	bacterioph	184	4	33.3	164	1	Y783_RHIME	P29953	rhizobium m
112	4	33.3	98	1	ELIA_PHYDR	P15571	phytophthor	185	4	33.3	165	1	Y4UD_RHISM	P55670	rhizobium s
113	4	33.3	98	1	ELIA_PHYME	P35696	phytophthor	186	4	33.3	165	1	YB09_MYCPN	P75453	mycoplasma s
114	4	33.3	98	1	ELIB_PHYCI	P35698	phytophthor	187	4	33.3	165	1	YREP_BUCTS	O31289	buchnera ap
115	4	33.3	98	1	ELIB_PHYDR	P35697	phytophthor	188	4	33.3	166	1	YREP_BUCRP	Q53016	buchnera ap
116	4	33.3	98	1	ELIB_PHYME	P35699	phytophthor	189	4	33.3	166	1	DIR_ENTFC	P00380	enterococcu
117	4	33.3	98	1	RL3E_SULAC	P11522	sulfolobus	190	4	33.3	167	1	NADM_METJA	Q57961	methanococc
118	4	33.3	104	1	YMF8_YEAST	Q04964	saccharomyc	191	4	33.3	167	1	UBC7_ARATH	P42747	arabidopsis
119	4	33.3	104	1	Y04A_BACAN	Q9RMV8	bacillus an	192	4	33.3	167	1	YREP_BUCAT	O92e0	buchnera ap
120	4	33.3	106	1	END4_THENE	O86954	thermotoga	193	4	33.3	167	1	YREP_BUCPP	O85061	buchnera ap
121	4	33.3	108	1	RL32_METH	O26128	methanobact	194	4	33.3	168	1	PBP_MANSE	Q92e24	buchnera ap
122	4	33.3	108	1	YPDH_ECOLI	P76525	escherichia	195	4	33.3	168	1	Y778_METJA	P18959	manduca sex
123	4	33.3	108	1	TH12_SYNV3	P73263	synecochyst	196	4	33.3	169	1	BMAE_ECOLI	Q58188	methanococc
124	4	33.3	109	1	Y091_BPP2	P33263	synecochyst	197	4	33.3	170	1	ENDA_METTH	O07165	methanobact
125	4	33.3	109	1	TH12_ANASP	P20857	anabaena sp	198	4	33.3	171	1	LACB_LACLA	P23495	lactococcu
126	4	33.3	110	1	VAG1_TOBAC	P06426	bacterioph	199	4	33.3	171	1	LACB_STRMO	P26424	streptococc
127	4	33.3	111	1	VAG2_TOBAC	P20857	anabaena sp	200	4	33.3	172	1	LECA_PLEWA	P23495	lactococcu
128	4	33.3	111	1	FERX_PSEPU	O82702	nicotiana t	201	4	33.3	172	1	Y074_NVPOP	O29988	pleurodeles
129	4	33.3	112	1	TRFF_BACME	P23103	pseudomonas	202	4	33.3	173	1	EGG1_SCHMA	O10327	argyia pseu
130	4	33.3	113	1	TRFF_BACME	Q57810	methanococc	203	4	33.3	173	1	HSCB_BUCAI	P06649	schistosoma
131	4	33.3	114	1	Y364_METJA	Q57810	methanococc	204	4	33.3	174	1	ARAI_ARAHY	P57659	buchnera ap
132	4	33.3	116	1	WN52_EPTST	P28120	epitretus	205	4	33.3	176	1	CYSC_SYNV3	P20780	arachis hyp
133	4	33.3	118	1	ELI1_PHYCR	P41802	phytophthor	206	4	33.3	177	1	EGG2_SCHMA	P72940	synecochyst
134	4	33.3	118	1	ELIB_PHYCR	P15570	phytophthor	207	4	33.3	177	1	EGG3_SCHMA	P12796	schistosoma
135	4	33.3	118	1	ELI_PHYCR	P41801	phytophthor	208	4	33.3	177	1	NUSG_BACSU	P13396	schistosoma
136	4	33.3	118	1	ELI_STAXY	P77986	staphylococ	209	4	33.3	177	1	NUSG_PSEAE	O06795	

253	4	33.3	199	1	UREG_HELPJ	Q92mz7 helicobacte	326	4	33.3	236	1	YJ94_ARCFU	O28285 archaeoglob
254	4	33.3	199	1	UREG_HELPY	Q90666 helicobacte	327	4	33.3	238	1	RK5_ODOSI	P49547 odontella s
255	4	33.3	200	1	DCG6_CHICK	O73770 gallus galli	328	4	33.3	239	1	REBE_YEREN	P456903 yersinia en
256	4	33.3	200	1	ITP1_HUMAN	O14713 homo sapien	329	4	33.3	239	1	YC27_CYAPA	P48259 cyanophora
257	4	33.3	200	1	ITP1_MOUSE	O35671 mus musculu	330	4	33.3	240	1	BAER_ECOLI	P30846 escherichia
258	4	33.3	200	1	TF21_MAIZE	P50158 zea mays (m	331	4	33.3	241	1	6PGL_TREPA	O83430 treponema p
259	4	33.3	201	1	RUVA_PSEAE	O51425 pseudomonas	332	4	33.3	241	1	HPB1_HAEIN	P35757 haemophilus
260	4	33.3	201	1	Y146_NPVAC	P41704 autographa	333	4	33.3	243	1	YC27_PORPU	P51358 porphyra pu
261	4	33.3	202	1	3MGH_STAM	Q99189 staphylococ	334	4	33.3	243	1	YEHW_ECOLI	P33359 escherichia
262	4	33.3	202	1	CD3E_CANFA	P27597 canis famil	335	4	33.3	244	1	YDZ1_SCHPO	O13709 schizosacch
263	4	33.3	202	1	COAE_CHLMU	Q9PJP9 chlamydia m	336	4	33.3	245	1	DAPB_MYCTU	P78024 mycobacteri
264	4	33.3	202	1	VANX_ENTFA	Q47749 enterococcu	337	4	33.3	245	1	HEX8_ADEG1	O89814 avian adeo
265	4	33.3	202	1	VANX_ENTFC	Q06241 enterococcu	338	4	33.3	245	1	PGY2_SYNEL	P50040 synchococc
266	4	33.3	203	1	RUVA_ECOLI	P08576 escherichia	339	4	33.3	246	1	GRPA_RAT	O81146 arabidopsis
267	4	33.3	203	1	YAL7_METJA	O58423 methanococc	340	4	33.3	246	1	PS61_ARATH	O81147 arabidopsis
268	4	33.3	204	1	YBM4_YEAST	P38068 saccharomyc	341	4	33.3	246	1	PS62_ARATH	O91147 arabidopsis
269	4	33.3	204	1	Y115_NPVAC	P41668 autographa	342	4	33.3	246	1	PSA6_ORISA	O91147 arabidopsis
270	4	33.3	205	1	FLRE_BOVIN	P52556 bos taurus	343	4	33.3	246	1	PSA6_SOYBN	O48551 glycine max
271	4	33.3	205	1	FLRE_HUMAN	P30043 homo sapien	344	4	33.3	246	1	PSA6_TOBAC	O9X977 nicotiana t
272	4	33.3	205	1	KTHY_PYRHO	O59366 pyrococcus	345	4	33.3	246	1	PGY2_ANASP	P29987 anabaena sp
273	4	33.3	206	1	EFA4_MOUSE	P11234 mus musculu	346	4	33.3	247	1	PGY2_MASLA	P29732 mastigoclad
274	4	33.3	206	1	RALB_HUMAN	P36860 rattus norv	347	4	33.3	248	1	YEGW_ECOLI	P76420 escherichia
275	4	33.3	206	1	RALB_RAT	P11234 mus musculu	348	4	33.3	249	1	SSAJ_SALTY	P74852 salmonella
276	4	33.3	206	1	T2D8_YEAST	Q12030 saccharomyc	349	4	33.3	250	1	DAPB_STRCO	O86836 streptomyce
277	4	33.3	206	1	YC10_ECOLI	P45847 escherichia	350	4	33.3	250	1	ETV3_HUMAN	P41162 homo sapien
278	4	33.3	207	1	CYOC_PSEPU	Q9WWR3 pseudomonas	351	4	33.3	250	1	YM25_ARCFU	O28058 archaeoglob
279	4	33.3	207	1	EGG2_SCHJA	P19469 schistosoma	352	4	33.3	252	1	PSA6_YEAST	P21243 saccharomyc
280	4	33.3	207	1	NOQ5_THETH	O56219 thermus aqu	353	4	33.3	253	1	RL2_YEAST	P29736 saccharomyc
281	4	33.3	207	1	YC10_HAEIN	P45303 haemophilus	354	4	33.3	254	1	AROD_NEIMB	Q9JYTO neisseria m
282	4	33.3	209	1	UPP_STRSL	P36399 streptococc	355	4	33.3	254	1	PT22_YEAST	P10355 saccharomyc
283	4	33.3	210	1	FLPA_HALNI	Q9HGG3 halobacteri	356	4	33.3	255	1	GLIC_MOUSE	Q9ESN4 mus musculu
284	4	33.3	211	1	CRB3_MOUSE	Q9JJJ9 mus musculu	357	4	33.3	255	1	YC27_GALSU	P28257 galdieria s
285	4	33.3	211	1	CRB3_RAT	O54424 rattus norv	358	4	33.3	256	1	KLK4_MOUSE	P00757 mus musculu
286	4	33.3	211	1	UREG_ACTPL	O54424 actinobacil	359	4	33.3	256	1	YQ11_CAEEL	P28257 galdieria s
287	4	33.3	212	1	EGG1_SCHJA	P19470 schistosoma	360	4	33.3	257	1	BLA2_BACSP	Q09503 caenorhabdi
288	4	33.3	212	1	ERP5_YEAST	P38819 saccharomyc	361	4	33.3	257	1	C1RF_HUMAN	P10425 bacillus sp
289	4	33.3	212	1	RA11_RHET	O54451 rhizobium e	362	4	33.3	258	1	C1RF_MOUSE	O75973 homo sapien
290	4	33.3	212	1	US01_HCMVA	P09714 human cytom	363	4	33.3	259	1	ETFB_CLOAB	O89992 mus musculu
291	4	33.3	212	1	Y331_MYCGE	P47573 mycoplasma	364	4	33.3	259	1	PGH1_BOVIN	P52040 clostridium
292	4	33.3	213	1	MOBE_THIFE	P22901 thiobacillu	365	4	33.3	259	1	DAPB_LACLA	O62664 bos taurus
293	4	33.3	214	1	COMA_BACSU	P14204 bacillus su	366	4	33.3	260	1	DHB8_MOUSE	Q9CFCO lactococcus
294	4	33.3	215	1	PIB_TREPA	O66105 treponema p	367	4	33.3	260	1	PT22_SACBA	P50171 mus musculu
295	4	33.3	216	1	KITH_STRCO	O50519 streptomyce	368	4	33.3	260	1	REFX_HUMAN	O13374 saccharomyc
296	4	33.3	217	1	B1OS_RHIME	O08250 rhizobium m	369	4	33.3	261	1	DHB8_HUMAN	Q92506 homo sapien
297	4	33.3	217	1	CAT_PROMI	P07641 proteus mir	370	4	33.3	261	1	TPIS_MYCTU	Q08408 mycobacteri
298	4	33.3	217	1	GTWU_CAVPO	P16413 cavia porce	371	4	33.3	261	1	YL82_CAEEL	P34440 caenorhabdi
299	4	33.3	217	1	NFNB_ECOLI	P15888 escherichia	372	4	33.3	261	1	IPYR_ARATH	P21216 arabidopsis
300	4	33.3	217	1	NHAB_PSEPU	P97052 pseudomonas	373	4	33.3	264	1	DAPB_BACHD	Q9K993 bacillus ha
301	4	33.3	217	1	THIE_HELPJ	O92101 helicobacte	374	4	33.3	265	1	APAL_PIG	P18648 sus scrofa
302	4	33.3	217	1	YGB9_METH	O26724 methanobact	375	4	33.3	265	1	MURI_PEDPE	Q08783 pediococcus
303	4	33.3	218	1	HRE1_NPVLD	Q90165 lymantria d	376	4	33.3	267	1	DAPB_BACFU	P42976 bacillus su
304	4	33.3	220	1	RAB3_DROME	P25228 drosophila	377	4	33.3	268	1	IF2A_ARCFU	O29723 archaeoglob
305	4	33.3	222	1	KCV_AQUAE	O67907 aquifex aeo	378	4	33.3	268	1	FA12_RHIME	P58381 rhizobium m
306	4	33.3	223	1	YGCY_ECOLI	P55139 escherichia	379	4	33.3	268	1	LGT_RICPR	Q9ZE99 rickettsia
307	4	33.3	224	1	GLBL_LAMSP	P16222 lamellibrac	380	4	33.3	268	1	MOV_P_TMV	P03583 tabacco mos
308	4	33.3	224	1	THY2_XENLA	Q00643 xenopus lae	381	4	33.3	268	1	MOV_P_TMV	P03583 tabacco mos
309	4	33.3	225	1	GTA_PLEPL	P30643 pleuronecte	382	4	33.3	268	1	MOV_P_TMV	P03583 tabacco mos
310	4	33.3	225	1	MINC_PASMU	P57845 pasteurella	383	4	33.3	268	1	MOV_P_TMV	P03583 tabacco mos
311	4	33.3	225	1	UREG_HAEIN	P44396 haemophilus	384	4	33.3	268	1	MOV_P_TMV	P03583 tabacco mos
312	4	33.3	227	1	UPP_HALNI	Q9Hn05 halobacteri	385	4	33.3	269	1	NIRC_ECOLI	P11097 escherichia
313	4	33.3	227	1	PYRF_METH	O26232 methanobact	386	4	33.3	269	1	NIRC_SALTY	P25936 salmonella
314	4	33.3	228	1	AOFB_BOVIN	P56560 bos taurus	387	4	33.3	269	1	REFX_MOUSE	Q92205 mus musculu
315	4	33.3	229	1	Y454_TREPA	O83467 treponema p	388	4	33.3	269	1	RM09_YEAST	P32134 saccharomyc
316	4	33.3	230	1	PVG_PORPU	P51365 porphyra pu	389	4	33.3	269	1	THID_HELPJ	Q92100 helicobacte
317	4	33.3	231	1	YHS2_YEAST	P38829 saccharomyc	390	4	33.3	270	1	PROB_LACLA	Q9CF72 lactococcus
318	4	33.3	231	1	YKRP_BACSU	P54443 bacillus su	391	4	33.3	270	1	THID_HELPY	O25515 helicobacte
319	4	33.3	232	1	NU5M_DICDI	Q34313 dictyosteli	392	4	33.3	270	1	YK77_ARCFU	O28202 archaeoglob
320	4	33.3	232	1	Y685_METH	O26781 methanobact	393	4	33.3	271	1	CPHB_SYNY3	P27383 synchocyst
321	4	33.3	233	1	HOKU_ALCEU	P22318 alcaligenes	394	4	33.3	271	1	PSB8_RAT	P28064 rattus norv
322	4	33.3	233	1	ICLN_CANFA	P35521 canis famil	395	4	33.3	271	1	YDJO_ECOLI	P76210 escherichia
323	4	33.3	235	1	NHAB_RHOSO	Q53117 rhodococcus	396	4	33.3	272	1	3DHQ_ACICA	Q59087 acinetobact
324	4	33.3	235	1	YCFE_BACSU	P37478 bacillus su	397	4	33.3	272	1	CYNT_SYNP7	P27134 synchococc
325	4	33.3	235	1			398	4	33.3	272	1	FAIL_RHIME	P58380 rhizobium m

399	4	33.3	1	PSB5_SCHPO	P30655	schizosacch	472	1	HEM3_THEAC	Q9hkm5	thermoplasm
400	4	33.3	1	TNR4_MOUSE	P47741	mus musculus	473	1	MPR1_SCHPO	O94321	schizosacch
401	4	33.3	1	ATPG_RAT	P35435	rattus norv	474	1	PNMT_MOUSE	P40935	mus musculus
402	4	33.3	1	RL2_RICPR	Q9zcq8	rickettsia	475	1	YRKH_BACSU	P54435	bacillus su
403	4	33.3	1	TO1A_CRICR	O9era9	cricketus cr	476	1	THYM_HUMAN	P25325	homo sapien
404	4	33.3	1	PSB5_ARATH	O23717	arabidopsis	477	1	BPHC_BURCE	P47228	burkholderi
405	4	33.3	1	US18_HCMVA	P09726	human cytom	478	1	DAPA_LACLA	Q9cf61	lactococcus
406	4	33.3	1	YAEF_ECOLI	P307056	escherichia	479	1	YIM4_YEAST	P40471	saccharomyc
407	4	33.3	1	YEU6_YEAST	P40072	saccharomyc	480	1	ATPG_BOVIN	P05631	bos taurus
408	4	33.3	1	YK22_CAEEL	P34324	caenorhabdi	481	1	YIHU_ECOLI	P32142	escherichia
409	4	33.3	1	IF2A_PYRHO	O9v0e4	pyrococcus	482	1	YK23_ARCFU	O28256	escherioglob
410	4	33.3	1	IF2A_PYRHO	O58655	pyrococcus	483	1	PRTM_LACLC	P36542	homo sapien
411	4	33.3	1	NRT1_RAT	P17982	rattus norv	484	1	ALFL_SYNP3	P14308	lactococcus
412	4	33.3	1	NRT2_RAT	P20974	rattus norv	485	1	ERA_MYCLE	Q07403	synecocyst
413	4	33.3	1	Y760_METJA	Q58170	methanococ	486	1	ERA_MYCLE	Q49768	mycobacteri
414	4	33.3	1	PSB8_HUMAN	P28062	homo sapien	487	1	KRBI_VACCC	P20505	vaccinia vi
415	4	33.3	1	PSB8_MOUSE	P28063	mus musculus	488	1	KRBI_VACCV	P16913	vaccinia vi
416	4	33.3	1	RL2_SYNP3	P73317	synecocyst	489	1	VG41_HSVI1	O00117	ictaluriid h
417	4	33.3	1	T1R1_RHOSH	P21763	rhodobacter	490	1	YF34_SYNP3	Q00117	ictaluriid h
418	4	33.3	1	LYTB_CAMJE	P15339	corynebacte	491	1	CHIA_ARATH	P74220	synecocyst
419	4	33.3	1	LYTB_CAMJE	P94644	campylobact	492	1	CHIA_ARATH	P08695	pseudomonas
420	4	33.3	1	MOVP_TAV	P23626	pyrococcus	493	1	LE29_GOSHI	P19172	arabidopsis
421	4	33.3	1	PNK_PYRHO	O58801	pyrococcus	494	1	LE29_GOSHI	P13940	gossypium h
422	4	33.3	1	YK23_ARCFU	P29986	anabaena sp	495	1	YF34_SYNP3	P57849	methanococc
423	4	33.3	1	YK23_ARCFU	P33018	escherichia	496	1	YF34_SYNP3	P41178	streptomyce
424	4	33.3	1	YK23_ARCFU	P29731	mastigoclad	497	1	YF34_SYNP3	Q9ku12	vibrio chol
425	4	33.3	1	YK23_ARCFU	Q92373	schizosacch	498	1	YF34_SYNP3	Q9ku12	vibrio chol
426	4	33.3	1	YK23_ARCFU	Q9yek6	aeropyrum p	499	1	YF34_SYNP3	Q9kcf0	bacillus ha
427	4	33.3	1	YK23_ARCFU	O29511	archaeoglob	500	1	YF34_SYNP3	Q9khl6	raistonia s
428	4	33.3	1	YK23_ARCFU	P19654	bacterioph	501	1	YF34_SYNP3	Q99549	homo sapien
429	4	33.3	1	YK23_ARCFU	P58866	xenopus lae	502	1	YF34_SYNP3	Q99549	homo sapien
430	4	33.3	1	YK23_ARCFU	O51743	borrelia bu	503	1	YF34_SYNP3	Q14180	schizosacch
431	4	33.3	1	YK23_ARCFU	P50576	brachydanio	504	1	YF34_SYNP3	Q14579	homo sapien
432	4	33.3	1	YK23_ARCFU	P19076	pseudomonas	505	1	YF34_SYNP3	P38974	paracoccus
433	4	33.3	1	YK23_ARCFU	Q03473	vibrio para	506	1	YF34_SYNP3	O59933	candida alb
434	4	33.3	1	YK23_ARCFU	Q92826	homo sapien	507	1	YF34_SYNP3	P27016	ommatstrephe
435	4	33.3	1	YK23_ARCFU	P54661	dictyosteli	508	1	YF34_SYNP3	P33360	escherichia
436	4	33.3	1	YK23_ARCFU	P75457	mycoplasma	509	1	YF34_SYNP3	P44195	haemophilus
437	4	33.3	1	YK23_ARCFU	P70321	mus musculus	510	1	YF34_SYNP3	P44195	haemophilus
438	4	33.3	1	YK23_ARCFU	Q9z9f0	heillobacill	511	1	YF34_SYNP3	P45476	escherichia
439	4	33.3	1	YK23_ARCFU	Q9wyj7	thermotoga	512	1	YF34_SYNP3	P28475	malus domes
440	4	33.3	1	YK23_ARCFU	P17981	mus musculus	513	1	YF34_SYNP3	P23641	saccharomyc
441	4	33.3	1	YK23_ARCFU	P42400	bacillus su	514	1	YF34_SYNP3	P45723	staphylococ
442	4	33.3	1	YK23_ARCFU	P50091	saccharomyc	515	1	YF34_SYNP3	P08128	oryctolagus
443	4	33.3	1	YK23_ARCFU	P34470	caenorhabdi	516	1	YF34_SYNP3	P55293	rhizobium s
444	4	33.3	1	YK23_ARCFU	Q09265	caenorhabdi	517	1	YF34_SYNP3	O19883	cyanidium c
445	4	33.3	1	YK23_ARCFU	P25914	mesocricetu	518	1	YF34_SYNP3	P22292	bos taurus
446	4	33.3	1	YK23_ARCFU	P54655	xenopus lae	519	1	YF34_SYNP3	Q02978	homo sapien
447	4	33.3	1	YK23_ARCFU	P37447	proteus vul	520	1	YF34_SYNP3	Q9cr62	mus musculus
448	4	33.3	1	YK23_ARCFU	Q51892	proteus mir	521	1	YF34_SYNP3	P97700	rattus norv
449	4	33.3	1	YK23_ARCFU	Q90x25	gallus gall	522	1	YF34_SYNP3	Q9krn5	vibrio chol
450	4	33.3	1	YK23_ARCFU	P32684	escherichia	523	1	YF34_SYNP3	P16565	rhodobacter
451	4	33.3	1	YK23_ARCFU	P18597	oryctolagus	524	1	YF34_SYNP3	O03047	nocardia la
452	4	33.3	1	YK23_ARCFU	P47231	rhodococcus	525	1	YF34_SYNP3	Q9uwr8	pyrococcus
453	4	33.3	1	YK23_ARCFU	P47477	mycoplasma	526	1	YF34_SYNP3	P95474	pyrococcus
454	4	33.3	1	YK23_ARCFU	P37730	thermoanaer	527	1	YF34_SYNP3	P44585	haemophilus
455	4	33.3	1	YK23_ARCFU	P52660	proteus vul	528	1	YF34_SYNP3	O78472	guillardia
456	4	33.3	1	YK23_ARCFU	O62246	caenorhabdi	529	1	YF34_SYNP3	Q9x235	thermotoga
457	4	33.3	1	YK23_ARCFU	P88083	human adeno	530	1	YF34_SYNP3	Q8kg83	vibrio chol
458	4	33.3	1	YK23_ARCFU	P57282	buchnera ap	531	1	YF34_SYNP3	O17795	caenorhabdi
459	4	33.3	1	YK23_ARCFU	P58057	escherichia	532	1	YF34_SYNP3	P14636	lupinus ang
460	4	33.3	1	YK23_ARCFU	P37768	escherichia	533	1	YF34_SYNP3	Q9qvx8	mus musculus
461	4	33.3	1	YK23_ARCFU	Q14165	homo sapien	534	1	YF34_SYNP3	P38123	saccharomyc
462	4	33.3	1	YK23_ARCFU	Q07264	zea luxuria	535	1	YF34_SYNP3	P38123	saccharomyc
463	4	33.3	1	YK23_ARCFU	P14171	rhodobacter	536	1	YF34_SYNP3	Q60080	vibrio mimi
464	4	33.3	1	YK23_ARCFU	P36910	beta vulgar	537	1	YF34_SYNP3	P78258	escherichia
465	4	33.3	1	YK23_ARCFU	Q08325	micromonosp	538	1	YF34_SYNP3	P14326	dictyosteli
466	4	33.3	1	YK23_ARCFU	Q9s3p9	vibrio angu	539	1	YF34_SYNP3	Q9y2d0	homo sapien
467	4	33.3	1	YK23_ARCFU	O46922	bacillus su	540	1	YF34_SYNP3	Q9qza0	mus musculus
468	4	33.3	1	YK23_ARCFU	Q04983	zymomonas m	541	1	YF34_SYNP3	P94463	bacillus su
469	4	33.3	1	YK23_ARCFU	P18598	rattus norv	542	1	YF34_SYNP3	Q92018	mus musculus
470	4	33.3	1	YK23_ARCFU	P72298	rhizobium m	543	1	YF34_SYNP3	Q59603	neisseria g
471	4	33.3	1	YK23_ARCFU	Q07159	staphylococ	544	1	YF34_SYNP3	P24084	vaccinia vi
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545	4	33.3	317	1	VB05_VACCL	P24083	vaccinia vi	618	4	33.3	346	1	LUXA_PHOPO	P24113	photobacter
546	4	33.3	317	1	VB05_VACCV	Q01227	vaccinia vi	619	4	33.3	347	1	ASRA_SALTY	P26474	salmonella
547	4	33.3	318	1	BCHC_RHOSH	Q02430	rhodobacter	620	4	33.3	347	1	EMRF_DROME	P10552	drosophila
548	4	33.3	318	1	ETFA_MYCLE	Q33096	mycobacteri	621	4	33.3	347	1	NTCI_RABIT	Q28727	o ileal sod
549	4	33.3	318	1	ETFA_MYCTU	O53275	mycobacteri	622	4	33.3	347	1	VP39_NPVAC	P17499	autographa
550	4	33.3	319	1	OTCA_BACSU	P18186	bacillus su	623	4	33.3	348	1	CHLI_EUGGR	P31205	euglena gra
551	4	33.3	320	1	CYF_CYAGA	O9t1s4	cyanidium c	624	4	33.3	348	1	NTCI_RAT	Q62633	r ileal sod
552	4	33.3	320	1	DDH_CORGL	P04964	corynebacte	625	4	33.3	350	1	RPOS_SHIFL	Q62633	r ileal sod
553	4	33.3	320	1	GSHB_SYNY3	P73493	synechocyst	626	4	33.3	351	1	MURG_HAEIN	P35540	shigelia fl
554	4	33.3	320	1	GUNE_RUMFL	Q05622	ruminococcu	627	4	33.3	351	1	PERX_SOLTU	P45065	haemophilus
555	4	33.3	320	1	STBA_ECOLI	P11904	escherichia	628	4	33.3	351	1	VA0D_HUMAN	P12437	solanum tub
556	4	33.3	321	1	ISP_BACCS	P29140	bacillus cl	629	4	33.3	351	1	VA0D_MOUSE	P12953	homo sapien
557	4	33.3	321	1	MMAL_DERFA	P16311	dermatophag	630	4	33.3	352	1	CYAB_STIAU	P51863	mus musculus
558	4	33.3	323	1	TRXB_AQUAE	O66790	aquifex aco	631	4	33.3	352	1	EGSA_THEAC	P40138	stigmatella
559	4	33.3	323	1	Y4LF_RHISN	P55546	rhizobium s	632	4	33.3	352	1	YC12_ARCFU	Q9h1j6	thermoplasm
560	4	33.3	323	1	YKCC_BACSU	Q34319	bacillus su	633	4	33.3	352	1	YMG7_YEAST	O29056	archaeoglob
561	4	33.3	324	1	ARGI_AGPT5	P14012	agrobacteri	634	4	33.3	353	1	CKR8_MOUSE	Q04651	saccharomyc
562	4	33.3	324	1	Y734_CHLPN	Q9z7h1	chlamydia p	635	4	33.3	353	1	GLNA_LOFLO	P56484	mus musculus
563	4	33.3	325	1	BIRA_BACSU	P42975	bacillus su	636	4	33.3	353	1	NUSG_THEMA	P52782	lupinus lut
564	4	33.3	325	1	MOCC_RHIME	P49304	rhizobium m	637	4	33.3	353	1	OP28_HAEIN	P29397	thermotoga
565	4	33.3	326	1	DUT_HSVB4	Q00030	equine herp	638	4	33.3	354	1	OP28_HAEIN	Q48221	haemophilus
566	4	33.3	326	1	DUT_HSVB4	P28892	equine herp	639	4	33.3	354	1	OP28_HAEIN	P09773	agrobacteri
567	4	33.3	326	1	LACD_LACLA	P26593	lactococcus	640	4	33.3	354	1	US28_HCMVA	P09704	human cytom
568	4	33.3	327	1	EBGR_ECOLI	P06846	escherichia	641	4	33.3	355	1	Y415_SYNY3	P22040	synchocyst
569	4	33.3	327	1	RPOA_MYCPN	Q50295	mycoplasma	642	4	33.3	355	1	GLN1_SOYBN	P24099	glycine max
570	4	33.3	327	1	YJIF_LACLA	Q9cgy0	lactococcus	643	4	33.3	355	1	GLN4_MAIZE	P38562	zea mays (m
571	4	33.3	328	1	NIR3_AZOBR	P45672	azospirillum	644	4	33.3	356	1	WN8D_HUMAN	Q9h1j5	homo sapien
572	4	33.3	328	1	RPOA_MYCGE	P74723	mycoplasma	645	4	33.3	356	1	GLN1_LOTJA	Q42899	lotus japon
573	4	33.3	328	1	YEO2_METJA	O58822	methanococc	646	4	33.3	356	1	GLN1_MEDSA	P04078	medicago sa
574	4	33.3	329	1	PLD1_HUMAN	O00151	homo sapien	647	4	33.3	356	1	GLN2_PHAVU	P04771	phaseolus v
575	4	33.3	329	1	PLC_BACCE	P14262	bacillus ce	648	4	33.3	356	1	GLN3_MAIZE	P38561	zea mays (m
576	4	33.3	329	1	PLC_BACTU	P08954	bacillus th	649	4	33.3	356	1	GLN3_PHAVU	P00965	phaseolus v
577	4	33.3	329	1	RBRS_ECOLI	P25551	escherichia	650	4	33.3	356	1	GLNA_NICPL	P12424	nicotiana p
578	4	33.3	330	1	GLK_BACHD	Q9kcz4	bacillus ha	651	4	33.3	356	1	GLNA_VIGAC	P32289	vigna acon
579	4	33.3	330	1	RPOS_ECOLI	P13445	escherichia	652	4	33.3	356	1	KARG_SCHAM	P91798	schistocerc
580	4	33.3	330	1	RPOS_SALTY	P37400	salmonella	653	4	33.3	357	1	YG3P_YEAST	P48239	saccharomyc
581	4	33.3	330	1	VP19_HSVSA	Q01051	herpesvirus	654	4	33.3	357	1	CHVE_AZOBR	P54083	azospirillu
582	4	33.3	331	1	GALR_SPTRR	Q9zbb1	streptococc	655	4	33.3	357	1	COBT_STRCO	Q9z8r1	streptomyce
583	4	33.3	331	1	LDHC_MOUSE	P00342	mus musculus	656	4	33.3	357	1	GLN1_MAIZE	P38559	zea mays (m
584	4	33.3	331	1	LDHC_MOUSE	P19629	rattus norv	657	4	33.3	357	1	GLN1_ORISA	P14654	oryza sativ
585	4	33.3	332	1	REGA_CLOSA	Q45831	clostridium	658	4	33.3	357	1	GLN3_PEA	Q43066	pisum sativ
586	4	33.3	332	1	YACO_ALCEU	Q9er39	mus musculus	659	4	33.3	358	1	GLN5_MAIZE	P38563	zea mays (m
587	4	33.3	333	1	TOIA_MOUSE	O9er39	mus musculus	660	4	33.3	358	1	GLNA_LACSA	P23712	lactuca sat
588	4	33.3	334	1	SCRR_KLEPN	P37076	klebsiella	661	4	33.3	358	1	SYFA_STRCO	P88055	streptomyce
589	4	33.3	334	1	SCRR_SALTY	P37077	salmonella	662	4	33.3	358	1	WNT8_XENLA	P28026	xenopus lae
590	4	33.3	334	1	Y052_RICPR	Q9ze55	rickettsia	663	4	33.3	359	1	OP21_HAEIN	P43839	haemophilus
591	4	33.3	335	1	DHFS_PIRAB	Q9v0n5	pyrococcus	664	4	33.3	359	1	TYD3_PAPSO	P54770	papaver som
592	4	33.3	335	1	VMAT_RINDR	P41358	rinderpest	665	4	33.3	359	1	WNSB_HUMAN	P22726	mus musculus
593	4	33.3	335	1	YF13_METJA	P45529	escherichia	666	4	33.3	360	1	WNSB_MOUSE	P22726	mus musculus
594	4	33.3	335	1	YHBM_ECOLI	Q55012	streptomyce	667	4	33.3	360	1	PURK_PSEAE	Q48216	haemophilus
595	4	33.3	336	1	PTLS_STRSO	Q27717	methanobact	668	4	33.3	360	1	VIS_AGRVI	P72158	pseudomonas
596	4	33.3	336	1	RLAO_METHH	P23247	vibrio chol	669	4	33.3	361	1	AROB_SYNT3	Q04554	agrobacteri
597	4	33.3	337	1	DHNS_VIBCH	Q98892	gallus gall	670	4	33.3	361	1	CCPR_YEAST	P73997	synechocyst
598	4	33.3	337	1	G55A_CHICK	Q9p445	cochliobolu	671	4	33.3	361	1	OP21_HAEIN	P00431	saccharomyc
599	4	33.3	337	1	MAT2_COCSA	Q9clv7	pasteurella	672	4	33.3	361	1	GMD1_ARATH	Q9snv3	arabidopsis
600	4	33.3	337	1	MENC_PASMU	Q76027	homo sapien	673	4	33.3	361	1	OP22_HAEIN	P20149	haemophilus
601	4	33.3	338	1	ANXG_HUMAN	Q44498	anabaena va	674	4	33.3	361	1	OP29_HAEIN	Q48217	haemophilus
602	4	33.3	338	1	CHLI_ANAVA	P55704	rhizobium s	675	4	33.3	361	1	Y101_NPVAC	P25655	autographa
603	4	33.3	338	1	Y4XL_RHISN	Q9x2a2	thermotoga	676	4	33.3	362	1	GCST_THEMA	P54378	bacillus su
604	4	33.3	339	1	ARGC_THENA	P55180	bacillus su	677	4	33.3	363	1	DIDR_CARAU	P35406	carassius a
605	4	33.3	339	1	GALE_BACSU	Q9un16	homo sapien	678	4	33.3	363	1	OP2B_HAEIN	Q48220	haemophilus
606	4	33.3	340	1	DUSC_HUMAN	Q06861	mycobacteri	679	4	33.3	363	1	TRMA_HAEIN	P31812	haemophilus
607	4	33.3	340	1	VIRS_MYCTU	P45540	escherichia	680	4	33.3	363	1	Y065_METJA	O60370	methanococc
608	4	33.3	340	1	YHFN_ECOLI	P78790	schizosacch	681	4	33.3	363	1	Y065_METJA	O60370	methanococc
609	4	33.3	341	1	ETFA_SCHPO	P32314	homo sapien	682	4	33.3	364	1	DCUP_RAT	Q926k1	chlamydia p
610	4	33.3	341	1	HTLF_HUMAN	P53112	saccharomyc	683	4	33.3	364	1	GCST_THEMA	P32362	rattus norv
611	4	33.3	341	1	PEXE_YEAST	Q9zed2	rickettsia	684	4	33.3	364	1	PERL_LYCES	Q9wv54	thermotoga
612	4	33.3	341	1	Y01L_RICPR	P57768	homo sapien	685	4	33.3	364	1	VMAT_NDVA	P15003	lycopersico
613	4	33.3	343	1	SNXG_HUMAN	P26935	bacillus su	686	4	33.3	364	1	VMAT_NDVB	P11206	newcastle d
614	4	33.3	344	1	MI2D_BACSU	Q28142	archaeoglob	687	4	33.3	365	1	DHAS_YEAST	P06157	newcastle d
615	4	33.3	344	1	SRBB_ARCFU	P57769	rattus norv	688	4	33.3	365	1	GCST_BACHD	P13663	saccharomyc
616	4	33.3	344	1	SNXG_RAT	P40830	bacillus su	689	4	33.3	365	1	YAGB_SCHPO	Q9k934	bacillus ha
617	4	33.3	345	1	PKSG_BACSU			690	4	33.3	366	1	TRMA_ECOLI	P23003	escherichia

691	4	33.3	366	1	TRMA_SALTY	P22038 salmonella	764	4	33.3	391	1	NCAP_ORSVW	Q83957 ovine respi
692	4	33.3	366	1	YCGT_ECOLI	P76015 escherichia	765	4	33.3	391	1	Y4CE_RHISN	P55387 rhizobium s
693	4	33.3	366	1	YG5F_YEAST	P53320 saccharomyc	766	4	33.3	392	1	GAT4_XENLA	Q91677 xenopus lae
694	4	33.3	366	1	YHK0_YEAST	P38772 saccharomyc	767	4	33.3	392	1	PAF2_BOVIN	P79106 bos taurus
695	4	33.3	367	1	DCUP_HUMAN	P06132 homo sapien	768	4	33.3	392	1	PAF2_HUMAN	Q99487 homo sapien
696	4	33.3	367	1	DCUP_MOUSE	P70697 mus musculu	769	4	33.3	392	1	PO14_NASV1	Q03272 nasonia vit
697	4	33.3	367	1	OP2A_HAEIN	Q48219 haemophilus	770	4	33.3	393	1	LOLC_HAEIN	P44252 haemophilus
698	4	33.3	367	1	SS81_YEAST	P40073 saccharomyc	771	4	33.3	394	1	CEGT_HUMAN	Q16739 homo sapien
699	4	33.3	368	1	GLN2_MAIZE	Q01912 phaseolus a	772	4	33.3	394	1	DXR_SYNY3	Q55663 synechocyst
700	4	33.3	368	1	MNN9_CANAL	P38560 zea mays (m	773	4	33.3	394	1	FTTU_BUCAI	Q31297 buchnera ap
701	4	33.3	368	1	Y105_YEAST	P53697 candida alb	774	4	33.3	394	1	PGK_BACSU	P40924 bacillus su
702	4	33.3	369	1	OP27_HAEIN	P40577 saccharomyc	775	4	33.3	395	1	UXUA_HAEIN	P44488 haemophilus
703	4	33.3	369	1	REF2_CHLTM	Q48218 haemophilus	776	4	33.3	395	1	PORA_PYRAB	Q9uy24 pyrococcus
704	4	33.3	369	1	REF2_CHLTR	P38105 chlamydia m	777	4	33.3	396	1	PORA_PYRHO	O73986 pyrococcus
705	4	33.3	369	1	DCUP_SCHPO	O84465 schizosacch	778	4	33.3	396	1	AGS_AGRRH	P27875 agrobacteri
706	4	33.3	370	1	CYS1_HORVU	P25249 hordeum vul	779	4	33.3	396	1	CATE_HUMAN	P14091 homo sapien
707	4	33.3	371	1	CYS1_MAIZE	Q10716 zea mays (m	780	4	33.3	396	1	ENPL_BACSH	Q03415 bacillus sp
708	4	33.3	371	1	DHA_MCTTU	P30234 mycobacteri	781	4	33.3	396	1	ISCS_RUMPL	O54055 ruminococcu
709	4	33.3	371	1	DUT_HSV11	P10234 herpes simp	782	4	33.3	396	1	PLSB_CUCMO	P10349 cucurbita m
710	4	33.3	371	1	OP25_HAEIN	P46027 haemophilus	783	4	33.3	397	1	PORA_PYRPU	Q51804 pyrococcus
711	4	33.3	371	1	PROJ_BACSU	O07509 bacillus su	784	4	33.3	397	1	DF3B_MYCSM	P52851 mycobacteri
712	4	33.3	371	1	YNEK_ECOLI	P76150 escherichia	785	4	33.3	397	1	Y636_METJA	Q58053 methanococc
713	4	33.3	371	1	DP3B_CAUCR	P48198 caulobacter	786	4	33.3	397	1	Y929_THEMEA	P56727 thermotoga
714	4	33.3	372	1	GMD2_VIBCH	Q48198 caulobacter	787	4	33.3	398	1	Y095_MYCGE	P47341 mycoplasma
715	4	33.3	372	1	GMD2_VIBCH	O60547 homo sapien	788	4	33.3	399	1	BM8A_MOUSE	P34821 mus musculu
716	4	33.3	372	1	GMD5_HUMAN	O60547 homo sapien	789	4	33.3	399	1	BM8B_MOUSE	P55105 mus musculu
717	4	33.3	373	1	CYS2_HORVU	P25250 hordeum vul	790	4	33.3	399	1	DF3B_MYCLE	P46387 mycobacteri
718	4	33.3	373	1	GMD4_ECOLI	P32054 escherichia	791	4	33.3	399	1	DF3B_MYCPA	Q91716 mycobacteri
719	4	33.3	373	1	GMD1_VIBCH	O69522 vibrio chol	792	4	33.3	399	1	Y874_HAEIN	P44067 haemophilus
720	4	33.3	373	1	REF2_AQUAE	O67695 aquifex aeo	793	4	33.3	399	1	YF07_METJA	Q58902 methanococc
721	4	33.3	374	1	CHLI_ANASP	P58571 anabaena sp	794	4	33.3	400	1	FTTU_HERAU	P42477 herpetosiph
722	4	33.3	376	1	ADHL_ORYSA	P20306 oryza sativ	795	4	33.3	400	1	ENO_HALMA	P29201 haloarcula
723	4	33.3	376	1	MURG_RICCN	O92158 rickettsia	796	4	33.3	400	1	ENPL_MESAU	P08712 mesocricetu
724	4	33.3	376	1	R51C_HUMAN	Q43502 homo sapien	797	4	33.3	400	1	ENPL_BPT4	P04519 bacterioph
725	4	33.3	376	1	SERC_MYCTU	O10534 mycobacteri	798	4	33.3	400	1	Y47B_DROME	P81922 drosophila
726	4	33.3	378	1	G1AA_BACSU	Q00828 bacillus su	799	4	33.3	400	1	PUR2_THEMEA	Q9x0x7 thermotoga
727	4	33.3	378	1	HRC4_SYNY3	P72795 synechocyst	800	4	33.3	401	1	ASSY_AQUAE	O67213 aquifex aeo
728	4	33.3	379	1	ADHL_HORVU	P00333 zea mays (m	801	4	33.3	401	1	PGK_SYNY3	P74421 synechocyst
729	4	33.3	379	1	ADHL_MAIZE	P14219 pennisetum	802	4	33.3	402	1	BMF8_HUMAN	P34820 homo sapien
730	4	33.3	379	1	LPXE_VIBCH	O9Kpw5 vibrio chol	803	4	33.3	402	1	C123_MYCTU	P77902 mycobacteri
731	4	33.3	379	1	METX_LEPME	P45493 campylobact	804	4	33.3	402	1	DP3B_MYCTU	Q50790 mycobacteri
732	4	33.3	379	1	Y2A6_PSEAE	P36797 human papil	805	4	33.3	402	1	F16P_SOYBN	Q42796 glycine max
733	4	33.3	381	1	GALM_ACICA	O18326 bombyx mori	806	4	33.3	402	1	RDS1_SCHPO	P53693 schizosacch
734	4	33.3	383	1	HIPO_CAMJE	P94891 leptospira	807	4	33.3	403	1	PGK_STRCO	Q9ze519 streptomyce
735	4	33.3	384	1	VE2_HPV53	Q51385 pseudomonas	808	4	33.3	404	1	ALR_RICPR	Q9ze52 rickettsia
736	4	33.3	384	1	HUNE_BOMMO	P05149 acinetobact	809	4	33.3	404	1	ISCS_NELMB	O91yy0 neisseria m
737	4	33.3	385	1	O82A_DROME	P45493 campylobact	810	4	33.3	404	1	Y256_METJA	O57706 methanococc
738	4	33.3	385	1	OP23_HAEIN	P36797 human papil	811	4	33.3	406	1	IDH_SPHYA	P50215 sphingomona
739	4	33.3	385	1	TP6A_AERPE	P28986 drosophila	812	4	33.3	406	1	METK_METJA	Q58605 methanococc
740	4	33.3	385	1	TRMU_UREPA	P46025 haemophilus	813	4	33.3	406	1	T23Q_MOUSE	P48776 mus musculu
741	4	33.3	385	1	TUD3_AGRVI	Q9ye67 aeropyrum p	814	4	33.3	406	1	T23Q_RAT	P42776 mus musculu
742	4	33.3	385	1	VATC_METTH	O9pq88 ureaplasma	815	4	33.3	406	1	YDLB_SCHPO	P21643 rattus norv
743	4	33.3	386	1	CRTY_ERWHE	P70788 agrobacteri	816	4	33.3	407	1	CGEI_CHICK	P87126 schizosacch
744	4	33.3	386	1	LMPI_EBVR	O27038 methanobact	817	4	33.3	407	1	F16P_PEA	P49707 gallus gall
745	4	33.3	386	1	LMPI_EBVR	Q01331 erwinia-bar	818	4	33.3	407	1	HEM1_RHOSH	P46275 pisum sativ
746	4	33.3	386	1	OP24_HAEIN	P03230 epstein-bar	819	4	33.3	407	1	YDAD_SCHPO	Q04512 rhodobacter
747	4	33.3	387	1	D4DR_MOUSE	P13198 epstein-bar	820	4	33.3	407	1	YEAD_SCHPO	O41078 schizosacch
748	4	33.3	387	1	D4DR_RAT	P46026 haemophilus	821	4	33.3	408	1	GCDH_PIG	P81140 sus scrofa
749	4	33.3	387	1	NWT_DROME	P51436 mus musculu	822	4	33.3	409	1	QCDH_CAEEL	Q20772 caenorhabdi
750	4	33.3	387	1	RT05_SCHPO	P30729 rattus norv	823	4	33.3	409	1	NQO4_THETH	O56220 thermus aqu
751	4	33.3	387	1	FLHF_BORBU	O61613 drosophila	824	4	33.3	409	1	TGF3_PIG	P15203 sus scrofa
752	4	33.3	388	1	PURK_SYNY3	Q44758 borrelia bu	825	4	33.3	410	1	PGLT_MAIZE	P35339 zea mays (m
753	4	33.3	388	1	TRPB_BUCAI	P74724 synechocyst	826	4	33.3	410	1	TGF3_MOUSE	P17125 mus musculu
754	4	33.3	388	1	TP6A_SULSH	O44685 buchnera ap	827	4	33.3	410	1	Y474_AQUAE	O66772 aquifex aeo
755	4	33.3	389	1	WNT4_DROME	O05208 sulfolobus	828	4	33.3	411	1	F16P_BRANA	P07204 brassica ap
756	4	33.3	389	1	GAT5_CHICK	P40589 drosophila	829	4	33.3	411	1	FOLC_BUCAI	P57265 buchnera ap
757	4	33.3	391	1	IDH_STRSL	P43692 gallus gall	830	4	33.3	411	1	GP18_YEAST	Q7265 buchnera na
758	4	33.3	391	1	IF43_NICPL	O5985 streptococc	831	4	33.3	412	1	AATC_BOVIN	P38703 saccharomyc
759	4	33.3	391	1	NCAP_BRSYA	P41380 nicotiana p	832	4	33.3	412	1	AATC_HORSE	P33097 bos taurus
760	4	33.3	391	1	NCAP_BRSVL	P22677 bovine resp	833	4	33.3	412	1	AATC_HUMAN	P08906 equus cabal
761	4	33.3	391	1	NCAP_HRSV1	Q65708 bovine resp	834	4	33.3	412	1	AATC_MOUSE	P17174 homo sapien
762	4	33.3	391	1	NCAP_HRSV1	P24566 human respi	835	4	33.3	412	1	AATC_PIG	P05201 mus musculu
763	4	33.3	391	1	NCAP_HRSVA	P03418 human respi	836	4	33.3	412	1		P00503 sus scrofa

837	4	33.3	412	1	AATC_RAT	P13221	rattus norv	910	4	33.3	439	1	VITL_DROME	P02843	drosophila
838	4	33.3	412	1	HOFO_ECOLI	P34749	escherichia	911	4	33.3	439	1	XVLA_CLONS	P29441	clostridium
839	4	33.3	412	1	IDH_ARCFU	O29610	archaeoglob	912	4	33.3	440	1	BRA2_BRAFL	P80492	brachiosteo
840	4	33.3	412	1	TGF2_CHICK	P30371	gallus gall	913	4	33.3	440	1	DNAA_THEMEA	P46798	thermotoga
841	4	33.3	412	1	TGF3_CHICK	P16047	gallus gall	914	4	33.3	440	1	V117_FOWPV	Q91545	fowlpox vir
842	4	33.3	412	1	TGF3_HUMAN	P10600	homo sapien	915	4	33.3	440	1	YGR4_YEAST	P53107	saccharomyc
843	4	33.3	412	1	TGF3_RAT	Q07258	rattus norv	916	4	33.3	441	1	MGTA_THEMEA	P80099	thermotoga
844	4	33.3	413	1	TGF2_XENLA	P17247	xenopus lae	917	4	33.3	443	1	FUTB_DROME	Q9V1C1	drosophila
845	4	33.3	414	1	OAT_PLAFLD	Q07805	plasmodium	918	4	33.3	443	1	GLNA_PYRHO	O38097	pyrococcus
846	4	33.3	414	1	RP54_HELPY	P56143	helicobacte	919	4	33.3	443	1	ZIC1_XENLA	O73689	xenopus lae
847	4	33.3	414	1	TGF2_HUMAN	P08112	homo sapien	920	4	33.3	444	1	BGLA_THENE	O33843	thermotoga
848	4	33.3	414	1	TGF2_MOUSE	P27090	mus musculus	921	4	33.3	444	1	TS57_MYCTU	Q10621	mycobacteri
849	4	33.3	415	1	Y232_RICPR	Q92du2	rickettsia	922	4	33.3	445	1	ACSC_MYCPN	O07340	mycoplasma
850	4	33.3	417	1	F16P_ARATH	P25851	arabidopsis	923	4	33.3	445	1	AMPY_MYCPN	P75206	mycoplasma
851	4	33.3	417	1	FTSA_PSEAE	P47203	pseudomonas	924	4	33.3	445	1	GUDX_ECOLI	P76637	escherichia
852	4	33.3	417	1	NAP1_YEAST	P25293	saccharomyc	925	4	33.3	445	1	NRH3_MOUSE	Q620Y9	mus musculus
853	4	33.3	417	1	SUCB_PIG	P53590	sus scrofa	926	4	33.3	445	1	NRH3_RAT	O22685	rattus norv
854	4	33.3	418	1	RHLB_HAEIN	P44922	haemophilus	927	4	33.3	445	1	PO21_POPJA	Q03273	popillia ja
855	4	33.3	419	1	RHLB_HAEIN	P35970	african swi	928	4	33.3	446	1	SHT_BOMBO	Q17239	bombyx mori
856	4	33.3	419	1	DNLI_ASEB7	P29299	pseudanabae	929	4	33.3	446	1	AP50_SCHPO	O08718	schizosacch
857	4	33.3	419	1	DNLI_ASEB7	P34283	caenorhabdi	930	4	33.3	446	1	BGLA_THEMEA	Q46915	escherichia
858	4	33.3	420	1	YKK6_CABEL	P22768	saccharomyc	931	4	33.3	446	1	GUDX_ECOLI	P52931	pseudomonas
859	4	33.3	420	1	ASSY_YEAST	Q58409	methanococc	932	4	33.3	446	1	HYIN_PSESY	P49742	schizosacch
860	4	33.3	420	1	LE21_METJA	Q17453	schistosoma	933	4	33.3	446	1	LPLD_BACSU	P47631	mycoplasma
861	4	33.3	420	1	PSD4_SCHMA	O17453	schistosoma	934	4	33.3	446	1	LPLD_BACSU	Q13133	homo sapien
862	4	33.3	420	1	PSD4_SCHMA	P29299	pseudanabae	935	4	33.3	446	1	TBAB_SCHCO	Q15915	homo sapien
863	4	33.3	421	1	SNAA_STRPR	P54991	streptomyce	936	4	33.3	447	1	AMPY_MYCCE	P46884	mus musculus
864	4	33.3	422	1	RHO_RHOSH	P25156	rhodobacter	937	4	33.3	447	1	NRH3_HUMAN	P26208	clostridium
865	4	33.3	423	1	PHS2_PHALU	O43617	phaseolus l	938	4	33.3	447	1	TBB1_MANSE	Q17134	branchiost
866	4	33.3	424	1	CBPT_THEVU	P29068	thermoactin	939	4	33.3	447	1	ZIC1_HUMAN	Q61312	mus musculus
867	4	33.3	424	1	LE22_METJA	P81291	methanococc	940	4	33.3	448	1	ZIC1_MOUSE	O58511	methanococc
868	4	33.3	425	1	Y655_ARCFU	O29602	archaeoglob	941	4	33.3	449	1	BGLA_CLOTM	Q57842	methanococc
869	4	33.3	426	1	BMP7_XENLA	P30886	xenopus lae	942	4	33.3	449	1	BRA1_BRAFL	O33595	staphylococ
870	4	33.3	426	1	G6PI_HALN1	O29602	archaeoglob	943	4	33.3	449	1	ENV2_ECOLI	P42903	mus musculus
871	4	33.3	426	1	RAD9_SCHPO	P26306	schizosacch	944	4	33.3	449	1	ENV2_SALTI	P41406	escherichia
872	4	33.3	427	1	CARP_RHIPU	P09177	rhizomucor	945	4	33.3	449	1	ENV2_SALTI	O89882	salmonella
873	4	33.3	427	1	KDTA_HAEIN	P44806	haemophilus	946	4	33.3	450	1	ENV2_ECOLI	P42206	pseudomonas
874	4	33.3	428	1	GSA_STAAU	O34092	staphylococ	947	4	33.3	450	1	ENV2_SALTI	P09573	influenza a
875	4	33.3	428	1	PHS1_PHALU	P80463	phaseolus l	948	4	33.3	451	1	GUDH_PSEPU	P09574	influenza a
876	4	33.3	429	1	ENO_PSEAE	Q9Hxz5	pseudomonas	949	4	33.3	451	1	NRAM_IACKQ	Q971P2	clostridium
877	4	33.3	429	1	ENO_THEMEA	P42848	thermotoga	950	4	33.3	451	1	NRAM_IACKQ	P32604	saccharomyc
878	4	33.3	429	1	SYN_THEAC	Q9Hks7	thermoplasm	951	4	33.3	451	1	Y512_CLOAB	O87705	caulobacter
879	4	33.3	429	1	URAA_ECOLI	P33780	escherichia	952	4	33.3	451	1	BMP5_MOUSE	P49994	staphylococ
880	4	33.3	430	1	BMP7_MOUSE	P23359	mus musculus	953	4	33.3	452	1	F26_YEAST	P22003	homo sapien
881	4	33.3	430	1	CD19_CAVPO	P225917	cavia porce	954	4	33.3	452	1	TIG_CAUCR	O26684	methanobact
882	4	33.3	430	1	MTSS_STAAU	P23737	staphylococ	955	4	33.3	452	1	DNAA_STAAU	P42238	bacillus su
883	4	33.3	430	1	SYN_BACHD	Q9Kc78	bacillus ha	956	4	33.3	453	1	BMP5_HUMAN	Q923R5	rhizobium m
884	4	33.3	430	1	VG49_BPFF1	P25130	bacterioph	957	4	33.3	454	1	CCA_METTH	P15169	homo sapien
885	4	33.3	431	1	BMP7_HUMAN	P18075	homo sapien	958	4	33.3	454	1	CCA_METTH	O28054	archaeoglob
886	4	33.3	431	1	SAHH_DROME	Q27580	drosophila	959	4	33.3	455	1	GUDH_BACSU	Q9KcJ2	bacillus ha
887	4	33.3	431	1	SAHH_MOUSE	P50247	mus musculus	960	4	33.3	455	1	AGLE_RHIME	P39868	escherichia
888	4	33.3	431	1	SAHH_RAT	P10760	rattus norv	961	4	33.3	458	1	CBFN_HUMAN	P39445	salmonella
889	4	33.3	431	1	SC65_RAT	Q64375	rattus norv	962	4	33.3	458	1	COBB_ARCFU	P30640	caenorhabdi
890	4	33.3	432	1	AGAR_LABOS	Q91081	labrus ossi	963	4	33.3	461	1	FTSY_AQUAE	P27350	streptomyce
891	4	33.3	432	1	AGSA_APLCA	P15287	aplysia cal	964	4	33.3	461	1	MYH_SCHPO	O67066	aquifex aeo
892	4	33.3	432	1	RAD9_SCHOT	P48013	schizosacch	965	4	33.3	462	1	CIXG_WEIPA	Q10159	schizosacch
893	4	33.3	432	1	RAD9_HUMAN	P23526	homo sapien	966	4	33.3	463	1	PPA2_SCHPO	Q9rlt3	w cixg pro
894	4	33.3	432	1	SPSK_BACSU	P39631	bacillus su	967	4	33.3	463	1	U140_DROME	Q01682	schizosacch
895	4	33.3	433	1	LE21_ARCFU	O28316	archaeoglob	968	4	33.3	464	1	CP85_LYCBS	Q9v784	drosophila
896	4	33.3	433	1	SAH1_XENLA	P51893	xenopus lae	969	4	33.3	464	1	DNAA_TREPA	Q43147	lycopersico
897	4	33.3	433	1	PYRD_ARATH	Q93477	xenopus lae	970	4	33.3	466	1	SELA_DESPA	O83047	treponema p
898	4	33.3	434	1	VG05_VAVCC	P21026	vaccinia vi	971	4	33.3	466	1	ZIC3_MOUSE	P56372	desulfovibr
899	4	33.3	434	1	VG05_VAVCC	P32955	variolela vir	972	4	33.3	466	1	ZIC3_MOUSE	Q9KcJ4	bacillus ha
900	4	33.3	434	1	SCB1_CAEEL	P29958	sus scrofa	973	4	33.3	467	1	D4DR_HUMAN	Q62521	mus musculus
901	4	33.3	435	1	TGF2_FIG	O67300	aquifex aeo	974	4	33.3	467	1	SVC_ARCFU	P21917	homo sapien
902	4	33.3	435	1	YC59_AQUAE	P04627	mus musculus	975	4	33.3	467	1	ZIC3_HUMAN	O29836	archaeoglob
903	4	33.3	436	1	KRAA_MOUSE	Q92791	homo sapien	976	4	33.3	467	1	ZIC3_HUMAN	O60481	homo sapien
904	4	33.3	437	1	NO55_HUMAN	P54743	mycobacteri	977	4	33.3	467	1	DHA7_SCHPO	P43353	homo sapien
905	4	33.3	437	1	PKNA_MYCLE	P27604	caenorhabdi	978	4	33.3	467	1	E2B8_SCHPO	P56288	schizosacch
906	4	33.3	437	1	SAHH_CAEEL	Q92947	homo sapien	979	4	33.3	468	1			
907	4	33.3	438	1	GCDH_HUMAN	Q60759	mus musculus	980	4	33.3	468	1			
908	4	33.3	438	1	GCDH_MOUSE			981	4	33.3	468	1			
909	4	33.3	438	1				982	4	33.3	468	1			

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Query Match          100.0%; Score 12; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
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DB 6 DAEFRHDSGYEV 17

RESULT 2
A4_URMSA STANDARD; PRT; 57 AA.
ID A4_URMSA
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
NCBI_TaxID=29073;
RX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56128; CAA39593.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57
FT SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DEFA CRC64;

Query Match          100.0%; Score 12; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
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DB 6 DAEFRHDSGYEV 17

RESULT 3
A4_CANFA STANDARD; PRT; 58 AA.
ID A4_CANFA
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
NCBI_TaxID=29073;
RX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56128; CAA39593.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57
FT SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DEFA CRC64;

Query Match          100.0%; Score 12; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
    |||||
DB 6 DAEFRHDSGYEV 17

RESULT 3
A4_CANFA STANDARD; PRT; 58 AA.
ID A4_CANFA
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
NCBI_TaxID=29073;
RX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
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RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
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CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
CC EMBL; X56128; CAA39593.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57
FT SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DEFA CRC64;

Query Match          100.0%; Score 12; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
    |||||
DB 6 DAEFRHDSGYEV 17

RESULT 3
A4_CANFA STANDARD; PRT; 58 AA.
ID A4_CANFA
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
NCBI_TaxID=29073;
RX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
CC EMBL; X56128; CAA39593.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57
FT SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DEFA CRC64;

Query Match          100.0%; Score 12; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
    |||||
DB 6 DAEFRHDSGYEV 17

RESULT 3
A4_CANFA STANDARD; PRT; 58 AA.
ID A4_CANFA
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia;
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AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GN Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; X56125; CAA39590.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
DR -----
DR EMBL; X56125; CAA39590.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
DR -----
Query Match 100.0%; Score 12; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEV 12
Db 7 DAEFRHDSGYEV 18
| | | | | | | | | | | | | | | | | |
RESULT 4
A4_RABIT
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GN Oryctolagus cuniculus (Rabbit).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56129; CAA39594.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
DR -----
Query Match 100.0%; Score 12; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEV 12
Db 6 DAEFRHDSGYEV 17
| | | | | | | | | | | | | | | | | |
RESULT 5
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GN Ovis aries (Sheep).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

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CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56126; CAA39591.1; -.
CC HSP; P05067; IBA4.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
CC
CC Query Match 100.0%; Score 12; DB 1; Length 58;
CC Best Local Similarity 100.0%; Pred. No. 1.7e-07;
CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 DAEFRHDSGYEV 12
CC DB 6 DAEFRHDSGYEV 17
CC
CC RESULT 6
CC A4_BOVIN
CC ID A4_BOVIN STANDARD; PRT; 59 AA.
CC AC Q28053;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 01-MAY-2000 (Rel. 39, Last annotation update)
CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
CC DE protein (Beta-App) (A-beta)] (Fragment).
CC GN APP.
CC OS Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Bovinae; Bos.
CC OX NCBI_TaxID=9913;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Brain;
CC RX MEDLINE=92010709; PubMed=1656157;
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
CC RT "Conservation of the sequence of the Alzheimer's disease amyloid
CC RT peptide in dog, polar bear and five other mammals by cross-species
CC RT polymerase chain reaction analysis."
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC CC G(O) (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC CC -----
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CC -----
CC EMBL; X56124; CAA39589.1; -.
CC HSP; P05067; IBA4.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
CC
CC Query Match 100.0%; Score 12; DB 1; Length 58;
CC Best Local Similarity 100.0%; Pred. No. 1.7e-07;
CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 DAEFRHDSGYEV 12
CC DB 6 DAEFRHDSGYEV 17
CC
CC RESULT 6
CC A4_BOVIN
CC ID A4_BOVIN STANDARD; PRT; 59 AA.
CC AC Q28053;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 01-MAY-2000 (Rel. 39, Last annotation update)
CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
CC DE protein (Beta-App) (A-beta)] (Fragment).
CC GN APP.
CC OS Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Bovinae; Bos.
CC OX NCBI_TaxID=9913;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Brain;
CC RX MEDLINE=92010709; PubMed=1656157;
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
CC RT "Conservation of the sequence of the Alzheimer's disease amyloid
CC RT peptide in dog, polar bear and five other mammals by cross-species
CC RT polymerase chain reaction analysis."
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC CC G(O) (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC CC -----
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CC -----
CC EMBL; X56124; CAA39589.1; -.
CC HSP; P05067; IBA4.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
CC
CC Query Match 100.0%; Score 12; DB 1; Length 59;
CC Best Local Similarity 100.0%; Pred. No. 1.7e-07;
CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 DAEFRHDSGYEV 12
CC DB 7 DAEFRHDSGYEV 18
CC
CC RESULT 7
CC A4_SAISC
CC ID A4_SAISC STANDARD; PRT; 751 AA.
CC AC Q95241;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
CC DE amyloid protein (Beta-App) (A-beta)].
CC GN APP.
CC OS Saimiri sciureus (Common squirrel monkey).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
CC OX NCBI_TaxID=9521;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Liver, and Kidney;
CC RX MEDLINE=96108492; PubMed=8532114;
CC RA Levy E., Amorim A., Frangione B., Walker L.C.;
CC RT "Beta-amyloid precursor protein gene in squirrel monkeys with
CC RT cerebral amyloid angiopathy."
CC RL Neurobiol. Aging 16:805-808(1995).
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC CC G(O).
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC CC WITH XII-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC CC PHOSPHORYLATION (BY SIMILARITY).
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC CC -----
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CC -----
CC EMBL; S81024; AAD14347.1; -.
CC HSP; P05067; IBA4.
CC InterPro; IPR001868; A4_APP.
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC
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DR EMBL; X56126; CAA39591.1; -.
DR HSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP. PARTIAL.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
DR KW Glycoprotein; Amyloid; Neurone; Transmembrane.
DR FT NON_TER 1 1
DR FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
DR FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
DR FT TRANSMEM 35 58 POTENTIAL.
DR FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
DR FT NON_TER 59 59
DR SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;
DR
DR Query Match 100.0%; Score 12; DB 1; Length 59;
DR Best Local Similarity 100.0%; Pred. No. 1.7e-07;
DR Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR
DR QY 1 DAEFRHDSGYEV 12
DR DB 7 DAEFRHDSGYEV 18
DR
DR RESULT 7
DR A4_SAISC
DR ID A4_SAISC STANDARD; PRT; 751 AA.
DR AC Q95241;
DR DT 15-DEC-1998 (Rel. 37, Created)
DR DT 15-DEC-1998 (Rel. 37, Last sequence update)
DR DT 16-OCT-2001 (Rel. 40, Last annotation update)
DR DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
DR DE amyloid protein (Beta-App) (A-beta)].
DR GN APP.
DR OS Saimiri sciureus (Common squirrel monkey).
DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
DR OX NCBI_TaxID=9521;
DR RN [1]
DR RP SEQUENCE FROM N.A.
DR RC TISSUE=Liver, and Kidney;
DR RX MEDLINE=96108492; PubMed=8532114;
DR RA Levy E., Amorim A., Frangione B., Walker L.C.;
DR RT "Beta-amyloid precursor protein gene in squirrel monkeys with
DR RT cerebral amyloid angiopathy."
DR RL Neurobiol. Aging 16:805-808(1995).
DR CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
DR CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
DR CC G(O).
DR CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
DR CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
DR CC WITH XII-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
DR CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
DR CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
DR CC PHOSPHORYLATION (BY SIMILARITY).
DR CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
DR CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
DR CC -----
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DR -----
DR EMBL; S81024; AAD14347.1; -.
DR HSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR
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DR PRINTS; PRO0759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
 Signal; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 17
 FT CHAIN 18 751
 FT CHAIN 653
 FT DOMAIN 18 680
 FT TRANSMEM 681 704
 FT DOMAIN 705 751
 FT DOMAIN 287 345
 FT SITE 740 743
 FT ACT_SITE 301 302
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 523 523
 FT CARBOHYD 552 552
 SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 12; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEV 12
 Db 653 DAEFRHDSGYEV 664
 |||||

RESULT 8
 ID A4_HUMAN STANDARD; PRT; 770 AA.
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
 DE (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
 GN APP OR A4 OR CVAP OR AD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Bewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid

RT is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 disease brain: coding and noncoding regions of the fetal precursor
 mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Pauridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 and partial sequence of a 4,200-dalton peptide isolated from cortical
 microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 gene.";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.

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RX MEDLINE=89384866; PubMed=2506449;
RX Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RX Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RX Sinha S.;
RX "The secreted form of the Alzheimer's amyloid precursor protein with
RX the Kunitz domain is protease nexin-II.";
RX Nature 341:144-147(1989).
RN [14]
RN PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=90211252; PubMed=1969731;
RX Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RX "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RX disease amyloid protein precursor.";
RX Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RN COMPLEX WITH G(O).
RX MEDLINE=93188965; PubMed=8446172;
RX Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
RX Murayama Y., Ogata E.;
RX "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RX protein G(O).";
RX Nature 362:75-79(1993).
RN [16]
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=99215582; PubMed=10201399;
RX Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
RX Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RX Parker M.W.;
RX "Crystal structure of the N-terminal, growth factor-like domain of
RX Alzheimer amyloid precursor protein.";
RX Nat. Struct. Biol. 6:327-331(1999).
RN [17]
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE=91104913; PubMed=2125487;
RX Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
RX "X-ray crystal structure of the protease inhibitor domain of
RX Alzheimer's amyloid beta-protein precursor.";
RX Biochemistry 29:10018-10022(1990).
RN [18]
RX STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031486; PubMed=1718421;
RX Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
RX Kanarok M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RX Tamburini P.P.;
RX "Sequential NMR resonance assignment and structure determination of
RX the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RX precursor protein.";
RX Biochemistry 30:10467-10478(1991).
RN [19]
RX STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RX Talafous J., Marcinkowski K.J., Klopman G., Zagorski M.G.;
RX "Solution structure of residues 1-28 of the amyloid beta-peptide.";
RX Biochemistry 33:7788-7796(1994).
RN [20]
RX STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RX Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RX "Three-dimensional structures of the amyloid beta peptide (25-35) in
RX membrane-mimicking environment.";
RX Biochemistry 35:16094-16104(1996).
RN [21]
RX STRUCTURE BY NMR OF 672-711.
RX MEDLINE=98359783; PubMed=9693002;
RX Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RX "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RX environment. Is the membrane-spanning domain where we think it is?";
RX Biochemistry 37:11064-11077(1998).
RN [22]
RX STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;
RX Poulsen S.A., Watson A.A., Craik D.J.;
RX "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site.";
RT J. Struct. Biol. 130:142-152(2000).
RN [23]
RX STRUCTURE BY NMR OF 681-706.
RX MEDLINE=20400065; PubMed=10940221;
RX Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
RX Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
RX "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RX water.";
RX J. Struct. Biol. 130:130-141(2000).
RN [24]
RX SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE=88296437; PubMed=2900137;
RX Dyrks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
RX Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RX "Identification, transmembrane orientation and biogenesis of the
RX amyloid A4 precursor of Alzheimer's disease.";
Query Match 100.0%; Score 12; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAERHDSGYEV 12
Db 672 DAERHDSGYEV 683
RESULT 9
AAT_STRGR AAT_STRGR STANDARD; PRT; 213 AA.
ID AC P36692;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable aspartate aminotransferase (EC 2.6.1.1) (Transaminase A)
DE (ASPART) (Fragment).
GN ASPC OR AATA.
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=94314177; PubMed=8039667; J.;
RX Kuberski S., Kasberg T., Distler J.;
RT "The nusg gene of Streptomyces griseus: cloning of the gene and
RT analysis of the A-factor binding properties of the gene product.";
RL FEMS Microbiol. Lett. 119:33-39(1994).
RN [2]
RN SEQUENCE OF 1-64 FROM N.A.
RC STRAIN=IFO 13350;
RX MEDLINE=94114580; PubMed=8286423;
RX Miyake K., Onaka H., Horinouchi S., Beppu T.;
RT "Organization and nucleotide sequence of the secE-nusG region of
RT Streptomyces griseus.";
RL Biochim. Biophys. Acta 1217:97-100(1994).
CC -!- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
CC L-glutamate.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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DR EMBL; X72787; CAA511294.1; -
DR EMBL; D17464; -; NOT_ANNOTATED_CDS.
DR PIR; S41059; S41059.
DR HSP; O56232; 1BJW.
DR InterPro; IPR001511; Aminotran_1.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; PARTIAL.
KW Transferase; Aminotransferase; Pyridoxal phosphate.
FT NON_TER 213 213
SQ SEQUENCE 213 AA; 22693 MW; C380BF59DA55A429 CRC64;

Query Match 50.0%; Score 6; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
|
Db 92 DSGYEV 97
|

RESULT 10
AAT_STRVG
ID AAT_STRVG STANDARD; PRT; 397 AA.
AC Q60013;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPART).
GN ASPC OR AAT.
OS Streptomyces virginiae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1961;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257210; PubMed=8675024;
RA Katayama M., Sakai Y., Okamoto S., Ihara F., Nihira T., Yamada Y.;
RA "Gene organization in the ada-rpL region of Streptomyces virginiae.";
RL Gene 171:135-136(1996).
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
L-glutamate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
CC
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CC
CC EMBL; D50624; BAA09299.1; -
CC HSP; Q56232; 1BJW.
CC InterPro; IPR001176; ACC_synthase.
CC InterPro; IPR001511; Aminotran_1.
CC Pfam; PF00155; aminotran_1_2; 1.
CC PRINTS; PR00753; ACCSYNTHASE.
CC PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Transferase; Aminotransferase; Pyridoxal phosphate.
FT BINDING 236 236 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 397 AA; 42381 MW; EEFEDCEB7D923065 CRC64;

Query Match 50.0%; Score 6; DB 1; Length 397;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
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Db 82 DSGYEV 87
|

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RESULT 11
EF1B_AERPE
ID EF1B_AERPE STANDARD; PRT; 90 AA.
AC Q9Y304;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Elongation factor 1-beta (EF-1-beta) (aEF-1beta).
GN EF1B OR APE2480.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1.
RX MEDLINE=93310339; PubMed=10382966;
RA Kwarababayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RA "Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -1- FUNCTION: PROMOTES THE EXCHANGE OF GDP FOR GTP IN EF-1-ALPHA/GDP.
THUS ALLOWING THE REGENERATION OF EF-1-ALPHA/GTP THAT COULD THEN
BE USED TO FORM THE TERNARY COMPLEX EF-1-ALPHA/GTP/AATRNA (BY
SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EF-1-BETA/EF-1-DELTA FAMILY.
CC
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CC
CC EMBL; AP000064; BAA81496.1; ALT_INIT.
CC InterPro; IPR001326; EF1BD.
CC Pfam; PF00736; EF1BD; 1.
CC Elongation factor; Protein biosynthesis; Complete proteome.
CC SEQUENCE 90 AA; 9885 MW; B7BCBC94013536F4 CRC64;
KW
SQ
Query Match 41.7%; Score 5; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
|
Db 32 SGYEV 36
|

RESULT 12
T2AH_DROME
ID T2AH_DROME STANDARD; PRT; 107 AA.
AC Q9W5B9;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Transcription initiation factor IIA gamma-2 chain (TFIIA-gamma-2).
GN TFIIA-S-2 OR EG:BACR7A4.7 OR CG11639.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

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Fri Sep 13 09:18:13 2002

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RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Aril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cleeve A., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.R., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: TFIIA IS A COMPONENT OF THE TRANSCRIPTION MACHINERY OF
CC RNA POLYMERASE II AND PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
CC ACTIVATION. INTERACTS WITH TBP (THE TATA-BINDING PROTEIN) (BY
CC SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER OF AN ALPHA (P30), A BETA (P20) AND A GAMMA
CC -!- SUBUNIT (P14) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE TFIIA-GAMMA FAMILY.
CC
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CC
CC -----
CC EMBL; AF003419; AAF45575.1; -.
CC HSSP; P32774; 1YTF.
CC FlyBase; FBgn0040338; TFIIA-S-2.
CC InterPro; IPR003194; TFIIA_gamma.
CC Pfam; PF02268; TFIIA_gamma.1.
CC Pfam; PF02751; TFIIA_gamma_C; 1.
CC Transcription regulation; Nuclear protein.
CC SEQUENCE 107 AA; 12273 MW; C6545CDDF3A65E44 CRC64;
CC
CC
CC Query Match 41.7%; Score 5; DB 1; Length 107;
CC Best Local Similarity 100.0%; Pred. No. 24;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC
CC RESULT 14
CC RS12_THETH
CC ID RS12_THETH STANDARD; PRT; 135 AA.
CC AC P17293;
CC DT 01-AUG-1990 (Rel. 15, Created)
CC DT 01-AUG-1990 (Rel. 15, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE 30S ribosomal protein S12.
CC GN RPSL OR RPS12.
CC OS Thermus aquaticus (subsp. thermophilus).
CC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.

```

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OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HBB / ATCC 27634;
RX MEDLINE=90301504; PubMed=2362824;
RA Yaknin A.V., Vorozheykina D.P., Matvienko N.I.;
RT "Nucleotide sequence of the Thermus thermophilus HB8 rps12 and rps7
RL genes coding for the ribosomal proteins S12 and S7.";
RN Nucleic Acids Res. 18:3659-3659(1990).
RN [2]
RP SEQUENCE OF 5-11.
RC STRAIN=VK1;
RX MEDLINE=92345325; PubMed=1637860;
RA Garber M.B., Agalarov S.C., Eliseikina I.A., Fomenkova N.P.,
RN Nikonov S.V., Sedelnikova S.E., Shikaeva O.S., Vasiliev D.,
RT Zhdanov A.S., Liljas A., Svensson L.A.;
RN "Ribosomal proteins from Thermus thermophilus for structural
RL investigations";
RN Biochimie 74:327-336(1992).
RN [3]
RP SEQUENCE OF 5-32.
RX MEDLINE=95045586; PubMed=7957245;
RA Tsioboli P., Herfurth E., Choli T.;
RT "Purification and characterization of the 30S ribosomal proteins from
RL the bacterium Thermus thermophilus.";
RN Eur. J. Biochem. 226:169-177(1994).
CC -!- FUNCTION: PROTEIN S12 IS INVOLVED IN THE TRANSLATION INITIATION
CC STEP.
CC -!- SIMILARITY: BELONGS TO THE S12P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; X52165; CAA36418.1; -
DR PIR; S10249; R3TW12.
DR InterPro; IPR000230; Ribosomal_S12.
DR Pfam; PF00164; Ribosomal_S12; 1.
DR PRINTS; PR01034; RIBOSOMALS12.
DR PRODOM; PD000576; Ribosomal_S12; 1.
DR PROSITE; PS00055; RIBOSOMAL_S12; 1.
DR KW Ribosomal protein.
FT CONFLICT 5 5 P -> V (IN REF. 2).
SQ SEQUENCE 135 AA; 1488 MW; 287BC5D2E36913B7 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SGYEV 12
Db 62 SGYEV 66

RESULT 15
ID YAF4_SCHPO STANDARD; PRT; 145 AA.
AC Q09858;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 16.8 kDa protein C29E6.04 in chromosome I.
CN SPAC29E6.04 OR SPAC30.08.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
NCBI_TaxID=4896;

Query Match 41.7%; Score 5; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SGYEV 12
Db 62 SGYEV 66
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Jones L., Murphy L., McNeill A., Simpson I., Harris D., Barrell B.G.,
RA Rajandream M.A., Walsh S.V.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA McDougall R.C., Rajandream M.A., Barrell B.G., Brown S., Murphy L.,
RA Jones L., McNeill A., Harris D.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Z66525; CAA91426.1; -
DR EMBL; ALI36538; CAB66467.1; -
DR HYPOHETICAL PROTEIN.
SQ SEQUENCE 145 AA; 16808 MW; 6FA7859AE1C93973 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 82 DAEFR 86

RESULT 16
RNK6_MIOTA STANDARD; PRT; 150 AA.
ID 046531;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Miopithecus.
OX NCBI_TaxID=36231;
RN [1]
RP SEQUENCE FROM N.A.
RA Deming M.S., Dyer K.D., Rosenberg H.F.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC -----
DR EMBL; AF037087; AAB94749.1; -
DR HSP; P00656; IL5Q.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Fc; 1.
```

DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Signal; Glycoprotein.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 150 RIBONUCLEASE K6.
 FT ACT_SITE 38 38 BY SIMILARITY.
 FT ACT_SITE 61 61 BY SIMILARITY.
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT DISULFID 46 104 BY SIMILARITY.
 FT DISULFID 60 114 BY SIMILARITY.
 FT DISULFID 78 129 BY SIMILARITY.
 FT DISULFID 85 92 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 150 AA; 17238 MW; 1595598C1750EEIC CRC64;

Query Match 41.7%; Score 5; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 32; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

QY 4 FRHDS 8
 |||||
 Db 66 FRHDS 70

RESULT 17
 YZCX_ECOLI STANDARD; PRT; 161 AA.
 AC P11291;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE very hypothetical 17.3 kba protein in cyaA region (CyaX) (O161).
 GN B3808.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OC
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92358234; PubMed=1379743;
 RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
 RT "Analysis of the Escherichia coli genome: DNA sequence of the region
 from 84.5 to 86.5 minutes."
 RL Science 257:771-778(1992).
 RN [2]
 RP SEQUENCE OF 1-116 FROM N.A.
 RX MEDLINE=85087947; PubMed=6393056;
 RA Aiba H., Mori K., Tanaka M., Ooi T., Roy A., Danchin A.;
 RT "The complete nucleotide sequence of the adenylate cyclase gene of
 Escherichia coli."
 RL Nucleic Acids Res. 12:9427-9440(1984).
 CC -!- CAUTION: THIS SEQUENCE, ACCORDING TO THE ECOSCO DATABASE (K. RUDD)
 IS PROBABLY NOT A REAL PROTEIN; THEREFORE THIS ENTRY WILL PROBABLY
 BE DELETED IN FUTURE RELEASES.

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 CC -----
 CC EMBL; M87049; AAA67604.1; -.
 CC EMBL; AE000456; AAC76811.1; -.
 CC EMBL; X01653; CAA25818.1; -.
 CC PIR; A30264; QOECCA.
 CC PIR; S30698; S30698.
 KW Hypothetical protein.
 SQ SEQUENCE 161 AA; 17342 MW; 84992F30086B3EA0 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 161;
 Best Local Similarity 100.0%; Pred. No. 34; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

QY 4 FRHDS 8
 |||||
 Db 98 FRHDS 102

RESULT 18
 COAT_SMLM STANDARD; PRT; 218 AA.
 ID COAT_SMLM
 AC P29151;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Coat protein.
 DE Coat protein.
 OS Satellite maize white line mosaic virus (SV-MMLMV).
 OC Viruses; Satellites.
 OC NCBI_TaxID=31503;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91111965; PubMed=1989380;
 RA Zhang L., Zitter T.A., Palukaitis P.;
 RT "Helper virus-dependent replication, nucleotide sequence and genome
 organization of the satellite virus of maize white line mosaic
 virus."
 RL Virology 180:467-473(1991).

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M55012; AAA47885.1; -.
 CC PIR; A38543; VCW2MW.
 CC HSP; P03606; 2STV.
 KW Coat protein.
 SQ SEQUENCE 218 AA; 23959 MW; 749079260147E068 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 218;
 Best Local Similarity 100.0%; Pred. No. 44; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

QY 8 SGYEV 12
 |||||
 Db 132 SGYEV 136

RESULT 19
 CD63_BOVIN STANDARD; PRT; 236 AA.
 ID CD63_BOVIN
 AC Q9XSK2; 2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE CD63 antigen.
 GN CD63.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Periphereal blood;
 RA Brooke G.P.;
 RT "The bovine homologue of CD63 is expressed at a high level on cattle

RT dendritic cells.";
 CC Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: MAY PLAY SOME ROLE IN SIGNAL TRANSDUCTION PATHWAYS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ012589; CAB40564.1; -;
 DR InterPro; IPR000301; Transmem_4;
 DR Pfam; PF00335; Transmembrane4; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Glycoprotein; Antigen; Transmembrane; Lysosome.
 FT INIT_MET 0
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 11 31 POTENTIAL.
 FT DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 51 69 POTENTIAL.
 FT DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 106 POTENTIAL.
 FT DOMAIN 107 201 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 202 222 POTENTIAL.
 FT DOMAIN 223 236 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 236 AA; 25648 MW; 91AF09A0B338CE09 CRC64;
 Query Match 41.7%; Score 5; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. NO. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 SGYEV 12
 Db 231 SGYEV 235
 RESULT 20
 CD63_HUMAN STANDARD; PRT; 237 AA.
 AC P08962;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE CD63 antigen (Melanoma-associated antigen ME491) (Lysosome-associated
 DE membrane glycoprotein 3) (LAMP-3) (Ocular melanoma-associated
 DE antigen) (OMA81H) (Granulophysin).
 GN CD63 OR ML41.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=88210273; PubMed=3365686;
 RA Hotta H., Ross A.H., Huebner K., Isobe M., Wendeborn S., Chao M.V.,
 RA Ricciardi R.P., Tsujimoto Y., Croce C.M., Koprowski H.;
 RT "Molecular cloning and characterization of an antigen associated with
 RT early stages of melanoma tumor progression.";
 RL Cancer Res. 48:2955-2962(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91131632; PubMed=1993697;
 KW Glycoprotein; Antigen; Transmembrane; Lysosome.

RA Metzelaar M.J., Wigngaard P.L., Peters P.J., Sixma J.J.,
 RA Nieuwenhuis H.K., Clevers H.C.;
 RT "CD63 antigen. A novel lysosomal membrane glycoprotein, cloned by a
 RT screening procedure for intracellular antigens in eukaryotic cells.";
 RL J. Biol. Chem. 266:3239-3245(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Ovary;
 RX MEDLINE=91025550; PubMed=2171551;
 RA Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,
 RA Scheit K.H.;
 RT "Characterization of three abundant mRNAs from human ovarian
 RT granulosa cells.";
 RL DNA Cell Biol. 9:479-485(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92287132; PubMed=1599482;
 RA Hotta H., Miyamoto H., Hara I., Takahashi N., Homma M.;
 RT "Genomic structure of the ME491/CD63 antigen gene and functional
 RT analysis of the 5'-flanking regulatory sequences.";
 RL Biochem. Biophys. Res. Commun. 185:436-442(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92181348; PubMed=1339263;
 RA Wang M.X., Earley J.J. Jr., Shields J.A., Donoso L.A.;
 RT "An ocular melanoma-associated antigen. Molecular characterization.";
 RL Arch. Ophthalmol. 110:399-404(1992).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lung, and Muscle;
 RA Strausberg R.;
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 1-20.
 RX MEDLINE=86049405; PubMed=4062294;
 RA Ross A.H., Dietzschold B., Jackson D.M., Earley J.J., Ghrist B.F.D.,
 RA Atkinson B., Koprowski H.;
 RT "Isolation and amino terminal sequencing of a novel
 RT melanoma-associated antigen.";
 RL Arch. Biochem. Biophys. 242:540-548(1985).
 CC -!- FUNCTION: THIS ANTIGEN IS ASSOCIATED WITH EARLY STAGES OF MELANOMA
 CC TUMOR PROGRESSION. MAY PLAY A ROLE IN GROWTH REGULATION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
 CC -!- TISSUE SPECIFICITY: DYSPLASTIC NEVI, RADIAL GROWTH PHASE PRIMARY
 CC MELANOMAS, HEMATOPOIETIC CELLS, TISSUE MACROPHAGES.
 CC -!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD63 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd63.htm".
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 CC -----
 DR EMBL; X07982; CAA30792.1; -;
 DR EMBL; M58485; -; NOT_ANNOTATED_CDS.
 DR EMBL; M59907; AAA63235.1; -;
 DR EMBL; X62654; CAA44519.1; -;
 DR EMBL; S93788; AAB21617.1; -;
 DR EMBL; BC002349; AAH02349.1; -;
 DR EMBL; BC013017; AAH13017.1; -;
 DR PIR; S01418; S01418.
 DR PIR; A39514; A39514.
 DR PIR; B35826; B35826.
 DR MIM; 155740; -;
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; Transmembrane4; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Glycoprotein; Antigen; Transmembrane; Lysosome.

Fri Sep 13 09:18:13 2002

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FT INIT_MET 0 0
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 POTENTIAL.
FT DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 69 POTENTIAL.
FT DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 106 POTENTIAL.
FT DOMAIN 107 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 223 POTENTIAL.
FT DOMAIN 224 237 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 237 AA; 25505 MW; 0C8C38F81CF0C9B CRC64;

Query Match 41.7%; Score 5; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
DB 232 SGYEV 236

RESULT 21
CD63_MOUSE STANDARD; PRT; 237 AA.
AC P41731;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD63 antigen.
GN CD63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94198294; PubMed=8148377;
RA Miyamoto M., Honma M., Hotta H.;
RT "Molecular cloning of the murine homologue of CD63/ME491 and
RT detection of its strong expression in the kidney and activated
RT macrophages."
RL Biochim. Biophys. Acta 1217:312-316(1994).
CC -!- FUNCTION: MAY PLAY SOME ROLE IN SIGNAL TRANSDUCTION PATHWAYS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
CC -----
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CC -----
CC EMBL; D16432; BAA03904.1; .
CC MGD; MGI:99529; Cd63.
CC InterPro; IPR000301; Transmem.4.
CC Pfam; PF00335; Transmembrane4; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1; 1.
CC Glycoprotein; Antigen; Transmembrane; Lysosome.
CC BY SIMILARITY.
CC INIT_MET 0 0
CC DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 11 31 POTENTIAL.
CC DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 51 69 POTENTIAL.
CC DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 81 106 POTENTIAL.
CC DOMAIN 107 202 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 203 223 POTENTIAL.
CC DOMAIN 224 237 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 237 AA; 25498 MW; 063454D727E9A36C CRC64;

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FT DOMAIN 107 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 223 POTENTIAL.
FT DOMAIN 224 237 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 237 AA; 25635 MW; 3C6EF16873B2A01C CRC64;

Query Match 41.7%; Score 5; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
DB 232 SGYEV 236

RESULT 22
CD63_RABIT STANDARD; PRT; 237 AA.
AC Q28709;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD63 antigen.
GN CD63.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95150837; PubMed=7820873;
RA Solma Y., Suzuki T., Sasano H., Nagura H., Nose M., Yamamoto T.;
RT "Increased mRNA for CD63 antigen in atherosclerotic lesions of
RT Watanabe heritable hyperlipidemic rabbits."
RL Cell Struct. Funct. 19:219-225(1994).
CC -!- FUNCTION: MAY PLAY SOME ROLE IN SIGNAL TRANSDUCTION PATHWAYS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC -!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
CC -----
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CC -----
CC EMBL; D21264; BAA04804.1; .
CC InterPro; IPR000301; Transmem.4.
CC Pfam; PF00335; Transmembrane4; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1; 1.
CC Glycoprotein; Antigen; Transmembrane; Lysosome.
CC BY SIMILARITY.
CC INIT_MET 0 0
CC DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 11 31 POTENTIAL.
CC DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 51 69 POTENTIAL.
CC DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 81 106 POTENTIAL.
CC DOMAIN 107 202 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 203 223 POTENTIAL.
CC DOMAIN 224 237 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 237 AA; 25498 MW; 063454D727E9A36C CRC64;

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Query Match          41.7%; Score 5; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
DB 232 SGYEV 236

RESULT 23
CD63_RAT
ID FABI_SYNY3 STANDARD; PRT; 237 AA.
AC P26648;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD63 antigen (AD1 antigen).
GN CD63.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92340890; PubMed=1634775;
RA Nishikata H., Oliver C., Mergenhagen S.E., Siraganian R.P.;
RT "The rat mast cell antigen AD1 (homologue to human CD63 or melanoma
RT antigen ME491) is expressed in other cells in culture.";
RL J. Immunol. 149:862-870(1992).
RN [2]
RP SEQUENCE OF 1-43.
RX MEDLINE=91107696; PubMed=1703138;
RA Kitani S., Berenstein E., Mergenhagen S.E., Tempst P.,
RA Siraganian R.P.;
RT "A cell surface glycoprotein of rat basophilic leukemia cells close
RT to the high affinity IgE receptor (Fc epsilon RI). Similarity to
RT human melanoma differentiation antigen ME491.";
RL J. Biol. Chem. 266:1903-1909(1991).
CC -1- FUNCTION: MAY BE INVOLVED IN THE SECRETORY PROCESS OF MAST CELLS
CC AND MAY PLAY SOME ROLE IN SIGNAL TRANSDUCTION PATHWAYS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC SECRETORY GRANULES AND PLASMA MEMBRANE OF MANY CULTURED CELL
CC LINES.
CC -1- TISSUE SPECIFICITY: ON MAST CELLS & PLATELETS OF RAT TISSUES.
CC INDUCED IN OTHER CELLS IN CULTURE.
CC -1- DEVELOPMENTAL STAGE: INCREASED EXPRESSION OF THE AD1 ANTIGEN IN
CC EMBRYONAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X61654; CAA43835.1;
DR PIR; S16776; S16776.
DR PIR; A46508; A46508.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4_1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1.
KW Glycoprotein; Antigen; Transmembrane; Lysosome.
FT INIT_MET 0
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 POTENTIAL.
FT DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 69 POTENTIAL.
FT DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 81 106 POTENTIAL.
FT DOMAIN 107 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 223 POTENTIAL.
FT DOMAIN 224 237 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 237 AA; 25567 MW; 3FE87E6DF3D72854 CRC64;

Query Match          41.7%; Score 5; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
DB 232 SGYEV 236

RESULT 24
FABI_SYNY3
ID FABI_SYNY3 STANDARD; PRT; 258 AA.
AC P73016;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-
DE dependent enoyl-ACP reductase).
GN FABI OR ENVM OR SLR1051.
OS Synechocystis sp. (strain PCC 6803).
CC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
CC NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima T., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Maruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-
CC 2,3-dehydroacyl-[acyl-carrier protein] + NADH.
CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90902; BAAL7036.1; ALT_INIT.
DR HSP; P29132; 1DFI.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00081; GDRDH.
KW Oxidoreductase; NAD; Fatty acid biosynthesis; Complete proteome.
FT NP_BIND 10 36 NAD (BY SIMILARITY).
SQ SEQUENCE 258 AA; 27626 MW; E912F0DF124FAE49 CRC64;

Query Match          41.7%; Score 5; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYE 11

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Fri Sep 13 09:18:13 2002

us-09-580-015-42_copy_1_12.oli.rsp

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Db 250 DSGYE 254

RESULT 25
ID T2S1_STRFI STANDARD; PRT; 269 AA.
AC 052512;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Type II restriction enzyme SfilI (EC 3.1.21.4) (Endonuclease SfilI)
DE (R.SfilI).
GN SFIIR.
OS Streptomyces fimbriatus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=68197;
RN [1]
RP SEQUENCE FROM N.A.
RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;
RT "Characterization of the SfilI restriction and modification genes.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DDAJ databases.
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGCNNNNNGGCC
CC AND CLEAVES BEFORE N-9.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
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CC -----
CC EMBL; AF039750; AAB95365.1; -
CC REBASE; 1655; SfilI.
CC HydroLase; Endonuclease; Nuclease; Restriction system.
CC SEQUENCE 269 AA; 31044 MW; 3C48499BAA5205EA CRC64;

Query Match 41.7%; Score 5; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 120 DAEFR 124

RESULT 26
ID PNMT_RAT STANDARD; PRT; 285 AA.
AC P10937;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phenylethanolamine N-methyltransferase (EC 2.1.1.28) (PNMTase)
DE (Noradrenaline N-methyltransferase).
DE GN PNMT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=95016700; PubMed=7931317;
RA Suh Y.H., Chun Y.S., Lee I.S., Kim S.S., Choi W., Chong Y.H.,
RA Hong L., Kim S.H., Park C.W., Kim C.G.;
RT "Complete nucleotide sequence and tissue-specific expression of the
rat phenylethanolamine N-methyltransferase gene.";

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J. Neurochem. 63:1603-1608(1994).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=WISTAR; TISSUE=Spleen;
RX MEDLINE=96035937; PubMed=7558218;
RA Koike G., Jacob H.J., Krieger J.E., Szpirer C., Hoehe M.R.,
RA Horiuchi M., Dzau V.J.;
RT "Investigation of the phenylethanolamine N-methyltransferase gene as
a candidate gene for hypertension.";
RL Hypertension 26:595-601(1995).
[3]
RN SEQUENCE OF 16-285 FROM N.A.
RP TISSUE=Adrenal gland;
RX MEDLINE=90135920; PubMed=2575695;
RA Weisberg E.P., Baruchin A., Stachowiak M.K., Stricker E.M.,
RA Zigmund M.J., Kaplan B.B.;
RT "Isolation of a rat adrenal cDNA clone encoding phenylethanolamine N-
methyltransferase and cold-induced alterations in adrenal PNMT mRNA
and protein.";
RL Brain Res. Mol. Brain Res. 6:159-166(1989).
[4]
RN SEQUENCE OF 26-285 FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=89183620; PubMed=2928117;
RA Mezey E.;
RT "Cloning of the rat adrenal medullary phenylethanolamine-N-
methyltransferase.";
RL Nucleic Acids Res. 17:2125-2125(1989).
CC -1- FUNCTION: CONVERTS NORADRENALINE TO ADRENALINE.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + phenylethanolamine =
CC S-adenosyl-L-homocysteine + N-methylphenylethanolamine.
CC -1- PATHWAY: LAST STEP IN CATECHOLAMINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE NNMT/PNMT/TEMT FAMILY.
CC -----
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CC -----
CC EMBL; X75333; CAA53082.1; -
CC EMBL; U11694; AAA91779.1; -
CC EMBL; U11275; AAA91779.1; JOINED.
CC EMBL; X14211; CAA32428.1; -
CC PIR; A60060; A60060.
CC PIR; S03614; S03614.
CC InterPro: IPR001601; Meth-transf.
CC InterPro: IPR000940; NNMT_PNMT_TEMT.
CC Pfam; PF01234; NNMT_PNMT_TEMT; 1.
CC PROSITE; PS01100; NNMT_PNMT_TEMT; 1.
CC Transferrase; Methyltransferase; Catecholamine biosynthesis.
CC CONFLICT 16 17 DS -> LA (IN REF. 3).
CC CONFLICT 52 52 D -> H (IN REF. 4).
CC CONFLICT 204 204 T -> A (IN REF. 4).
CC CONFLICT 211 211 N -> H (IN REF. 2 AND 3).
CC CONFLICT 214 214 F -> L (IN REF. 2 AND 3).
CC CONFLICT 285 285 V -> A (IN REF. 2).
CC SEQUENCE 285 AA; 31670 MW; 28A239A5411AD2F6 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 285;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
Db 247 SGYEV 251

RESULT 27
AMPM_CHLMU

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ID AMPM_CHLMU STANDARD; PRT; 291 AA.
 AC Q9PL68;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Methionine aminopeptidase (EC 3.4.11.18) (MAP) (Peptidase M).
 GN MAP OR TC0240.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MoPn / N199;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J.K., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.,
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC -1- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
 CC PROTEINS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)O = L-METHIONINE +
 CC PEPTIDE.
 CC -1- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT, SODIUM; BINDS 1 ION
 CC PER SUBUNIT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24A; ALSO KNOWN AS THE
 CC MAP FAMILY 1.
 CC
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 CC
 CC EMBL: AE002291; AAF39111.1; ALT_INIT.
 CC TIGR: TC0240;
 CC InterPro: IPR002457; MAP_1.
 CC InterPro: IPR001714; Methamino_Ptase.
 CC InterPro: IPR000994; Peptidase_M24.
 CC InterPro: IPR004027; SEC-C.
 CC Pfam: PF00557; Peptidase_M24; 1.
 CC Pfam: PF02810; SEC-C_1.
 CC PRINTS: PR00599; MAPEPTIDASE.
 CC PROSITE: PS00680; MAP_1; 1.
 CC Hydrolyase; Aminopeptidase; Cobalt; Complete proteome.
 KW METAL 135
 FT METAL 135 COBALT 2 (BY SIMILARITY).
 FT METAL 146 COBALT 1 AND 2 (BY SIMILARITY).
 FT METAL 209 COBALT 1 (BY SIMILARITY).
 FT METAL 241 COBALT 1 (BY SIMILARITY).
 FT METAL 273 COBALT 1 AND 2 (BY SIMILARITY).
 SQ SEQUENCE 291 AA; 32646 MW; BAA33E190FC6160E CRC64;

Query Match 41.7%; Score 5; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYE 11
 |||||
 Db 280 DSGYE 284

RESULT 28

ATHB_MOUSE
 ID ATHB_MOUSE STANDARD; PRT; 294 AA.
 AC P50992;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Potassium-transporting ATPase beta chain (Proton pump beta chain)
 DE (Gastric H+/K+ ATPase beta subunit).
 GN ATPAB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=92112757; PubMed=1370459;
 RA Morley G.P., Callaghan J.M., Rose J.B., Toh H., Gleeson P.A.,
 RA van Driel I.R.;
 RT "The mouse gastric H,K-ATPase beta subunit. Gene structure and co-
 RT ordinate expression with the alpha subunit during ontogeny.";
 RL J. Biol. Chem. 267:1165-1174(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=91376121; PubMed=1654563;
 RA Canfield V.A., Levenson R.;
 RT "Structural organization and transcription of the mouse gastric H+,
 RT K(+)-ATPase beta subunit gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8247-8252(1991).
 CC -1- SUBUNIT: COMPOSED OF TWO SUBUNITS: ALPHA (CATALYTIC) AND BETA.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE NA+/K+ AND H+ ATPASES BETA CHAIN
 CC FAMILY.

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 CC

EMBL: M80251; AAA37270.1;
 EMBL: M80247; AAA37270.1; JOINED.
 EMBL: M80248; AAA37270.1; JOINED.
 EMBL: M80249; AAA37270.1; JOINED.
 EMBL: M80250; AAA37270.1; JOINED.
 EMBL: M64688; AAA37269.1;
 EMBL: M64685; AAA37269.1; JOINED.
 EMBL: M64686; AAA37269.1; JOINED.
 EMBL: M64687; AAA37269.1; JOINED.
 MGD; MGI:88114; Atp4b.
 DR InterPro: IPR000402; Na_K_beta.
 DR Pfam: PF00287; Na_K-ATPase; 1.
 DR PROSITE: PS00390; ATPASE_NA_K_BETA_1; 1.
 DR PROSITE: PS00391; ATPASE_NA_K_BETA_2; 1.
 KW Potassium transport; Hydrogen ion transport; Transmembrane;
 KW Glycoprotein; Signal-anchor.
 FT DOMAIN 1 36
 FT TRANSMEM 37 57
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 99 99
 FT CARBOHYD 103 103
 FT CARBOHYD 130 130
 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 193 193
 FT CARBOHYD 225 225
 FT CARBOHYD 294 AA; 33566 MW; EAB8526C4C52431D CRC64;

Query Match 41.7%; Score 5; DB 1; Length 294;
 Best Local Similarity 100.0%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRR 6
|||||
Db 15 AEFRR 19

RESULT 29
ID PYRB_LACIA STANDARD; PRT; 310 AA.
AC O9CF79;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase).
DE PYRB OR LLI1602.
GN Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OS Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jaillon O., Malarne K.,
RT Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403";
RL Genome Res. 11:731-753(2001).
CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
+ N-carbamoyl-L-aspartate.
CC -1- PATHWAY: SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.

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CC EMBL: AE006390; AAK05700.1; -
CC InterPro: IPR002029; Carbmyltransf_asor.
DR Pfam: PF00185; OTCase; 1.
DR Pfam: PF02729; OTCase.N; 1.
DR PRINTS: PR00100; AOTCASE.
DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
KW Pyrimidine biosynthesis; Transferease; Complete proteome.
SQ SEQUENCE 310 AA; 34558 MW; EEDE6B8EC6F00B94 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHDSG 9
|||||
Db 229 RHDSG 233

RESULT 30
ID IKBA_PIG STANDARD; PRT; 314 AA.
AC Q08353;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NF-kappaB inhibitor alpha (I-kappa-B-alpha) (IkappaBalpha) (IKB-alpha)
(EC1-5).
GN NFkBIA OR IKBA.
OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=93327766; PubMed=8334993;
RA De Martin R., Vanhove B., Cheng Q., Hofer E., Csizmadia V.,
RA Winkler H., Bach F.H.;
RT "Cytokine-inducible expression in endothelial cells of an IkappaB
alpha-like gene is regulated by NF-kappaB";
RL EMBO J. 12:2773-2779(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137398; PubMed=7835710;
RA De Martin R., Holzmüller H., Hofer E., Bach F.H.;
RT "Intron-exon structure of the porcine IkappaB alpha-encoding gene.";
RL Gene 152:253-255(1995).
CC -1- FUNCTION: INHIBITOR OF NF-KAPPA-B THAT TIGHTLY REGULATES NF-KAPPA-
B ACTIVATION BY COMPLEXING AND TRAPPING IT IN THE CYTOSOL. MAY
BE INVOLVED IN REGULATION OF TRANSCRIPTIONAL RESPONSES TO NF-
KAPPA-B, INCLUDING CELL ADHESION, IMMUNE AND PROINFLAMMATORY
RESPONSES, APOPTOSIS, DIFFERENTIATION AND GROWTH. CONTROLLED BY
SEQUENTIAL SERINE-PHOSPHORYLATION, UBIQUITINATION AND DEGRADATION.
CC TYROSINE-PHOSPHORYLATION COULD ONLY LEAD TO DISSOCIATION FROM NF-
KAPPA-B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH P65 (RELA) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: SUBSEQUENT TO STIMULUS-DEPENDENT PHOSPHORYLATION ON SERINES,
POLYUBQUITINATION TARGETS THE PROTEIN FOR RAPID DEGRADATION VIA
THE UBIQUITIN SYSTEM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NF-KAPPA-B INHIBITOR FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.

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CC EMBL: Z21968; CAA79979.1; -
CC EMBL: Z35483; CAA84619.1; -
CC HSP; P25963; INFI.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 5.
DR PRINTS: PR01415; ANKYRIN.
DR SMART: SM00248; ANK; 3.
DR PROSITE: PS50088; ANK_REPEAT; 3.
DR PROSITE: PS0297; ANK_REPEAT_REGION; 1.
KW Phosphorylation; ANK repeat; Repeat; Ubiquitin conjugation.
FT REPEAT 110 139 ANK 1.
FT REPEAT 143 172 ANK 2.
FT REPEAT 182 211 ANK 3.
FT REPEAT 216 245 ANK 4.
FT BINDING 21 21 UBIQUITIN (BY SIMILARITY).
FT BINDING 22 22 UBIQUITIN (BY SIMILARITY).
FT MOD_RES 32 32 PHOSPHORYLATION (BY IKKA AND IKKB) (BY
SIMILARITY).
FT MOD_RES 36 36 PHOSPHORYLATION (BY IKKA, IKKB AND IKKE)
(BY SIMILARITY).
FT MOD_RES 42 42 PHOSPHORYLATION (BY TYR-KINASES)
(BY SIMILARITY).
FT SEQUENCE 314 AA; 35230 MW; 629BEDB824562E95 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHDSG 9
|||||

Db 29 RHDG 33

RESULT 31

IKBA_RAT
ID IKBA_RAT STANDARD; PRT; 314 AA.
AC Q63746;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NF-kappaB inhibitor alpha (I-kappa-B-alpha) (IkappaBalpha) (IKB-alpha)
DE (RL/IF-1).
GN NFkBIA OR IKBA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92158672; PubMed=1741294;
RT Tewari M., Mohn K.L., Yue F.E., Taub R.A.;
RA "Sequence of rat RL/IF-1 encoding an IkappaB, and comparison with
related proteins containing notch-like repeats.";
RL Nucleic Acids Res. 20:607-607(1992).
RN [2]
RP ERRATUM.
RA Tewari M., Mohn K.L., Yue F.E., Taub R.A.;
RL Nucleic Acids Res. 20:2624-2624(1992).
RN [3]
RP ERRATUM.

Tewari M., Mohn K.L., Yue F.E., Taub R.A.;
RL Nucleic Acids Res. 20:2931-2931(1992).
CC -1- FUNCTION: INHIBITOR OF NF-KAPPA-B THAT TIGHTLY REGULATES NF-KAPPA-
B ACTIVATION BY COMPLEXING AND TRAPPING IT IN THE CYTOPLASM. MAY
BE INVOLVED IN REGULATION OF TRANSCRIPTIONAL RESPONSES TO NF-
KAPPA-B, INCLUDING CELL ADHESION, IMMUNE AND PROINFLAMMATORY
RESPONSES, APOPTOSIS, DIFFERENTIATION AND GROWTH. CONTROLLED BY
SEQUENTIAL SERINE-PHOSPHORYLATION, UBIQUITINATION AND DEGRADATION.
CC TYROSINE-PHOSPHORYLATION COULD ONLY LEAD TO DISSOCIATION FROM NF-
KAPPA-B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH P65 (RELA) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: SUBSEQUENT TO STIMULUS-DEPENDENT PHOSPHORYLATION ON SERINES,
POLYUBIQUITINATION TARGETS THE PROTEIN FOR RAPID DEGRADATION VIA
THE UBIQUITIN SYSTEM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NF-KAPPA-B INHIBITOR FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.

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EMBL; X63594; CAA45138.1; -
DR HSSP; P25963; 1LN.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR PRINTS; PR01415; ANKYRN.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50086; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Phosphorylation; ANK repeat; Repeat; Ubiquitin conjugation.
FT REPEAT 110 139 ANK 1.
FT REPEAT 143 172 ANK 2.
FT REPEAT 182 211 ANK 3.
FT REPEAT 216 245 ANK 4.
FT BINDING 21 21 UBIQUITIN (BY SIMILARITY).
FT BINDING 22 22 UBIQUITIN (BY SIMILARITY).
FT MOD_RES 32 32 PHOSPHORYLATION (BY IKKA AND IKKB) (BY
SIMILARITY).

FT MOD_RES 36 36 PHOSPHORYLATION (BY IKKA, IKKB AND IKKE)
FT (BY SIMILARITY).
FT MOD_RES 42 42 PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 314 AA; 35017 MW; CC4C9D0F6CDDA950 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RHDG 9
Db 29 RHDG 33

RESULT 32
IKBA_HUMAN
ID IKBA_HUMAN STANDARD; PRT; 317 AA.
AC P25963;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE NF-kappaB inhibitor alpha (Major histocompatibility complex enhancer-
binding protein MAD3) (I-kappa-B-alpha) (IkappaBalpha) (IKB-alpha).
GN NFkBIA OR NFkB1 OR MAD3 OR IKBA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=91292530; PubMed=1829648;
RA Haskill S., Beg A.A., Tompkins S.M., Morris J.S., Yurochko A.D.,
Sampson-Johannes A., Mondal K., Ralph P., Baldwin A.S. Jr.;
RT "Characterization of an immediate-early gene induced in adherent
monocytes that encodes I kappa B-like activity.";
RL Cell 65:1281-1289(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=20105364; PubMed=10637284;
RA Jungnickel B., Staratschek-Jox A., Braeuninger A., Spleker T.,
Wolf J., Diehl V., Hansmann M.-L., Rajewsky K., Kueppers R.;
RT "Clonal deleterious mutations in the IkappaB alpha gene in the
malignant cells in Hodgkin's lymphoma.";
RL J. Exp. Med. 191:395-402(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Liu B., Huang A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and kidney;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP MUTAGENESIS OF K-21; K-22; D-31; S-32; D-35; T-36; S-243; S-262 AND
T-263.
RX MEDLINE=96239483; PubMed=8657102;
RA DiDonato J.A., Mercurio F., Rosette C., Wu-Li J., Suyang H., Ghosh S.,
Karin M.;
RT "Mapping of the inducible IkappaB phosphorylation sites that signal
its ubiquitination and degradation.";
RL Mol. Cell. Biol. 16:1295-1304(1996).
RN [6]
RP PHOSPHORYLATION OF TYR-42, AND MUTAGENESIS OF TYR-42.
RX MEDLINE=96390852; PubMed=8797825;
RA Imbert V., Rupec R.A., Livolsi A., Pahl H.L., Traenckner E.B.-M.,
Mueller-Dieckmann C., Farahfar D., Rossi B., Auberger P.,
Baeuerle P.A., Peyron J.-F.;
RT "Tyrosine phosphorylation of IkappaB-alpha activates NF-kappaB without

RT proteolytic degradation of IkappaB-alpha.;

RL Cell 86:787-798(1996).

RR [7]

RP PHOSPHORYLATION OF SER-32 AND SER-36.

RX MEDLINE=20337984; PubMed=10892136;

RA Peters R.T., Liao S.-M., Maniatis T.;

RT "IKK epsilon is part of a novel PMA-inducible IkappaB kinase

RT complex.";

RL Mol. Cell 5:513-522(2000).

RR [8]

RN UBIQUITINATION OF LYS-21 AND LYS-22.

RP MEDLINE=96074687; PubMed=7479976;

RX Scherer D.C., Brockman J.A., Chen Z., Maniatis T., Ballard D.W.;

RA "Signal-induced degradation of IkappaB alpha requires site-specific

RT ubiquitination.";

RT Proc. Natl. Acad. Sci. U.S.A. 92:11259-11263(1995).

RL [9]

RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 70-282.

RP MEDLINE=99081291; PubMed=9865693;

RX Jacobs M.D., Harrison S.C.;

RA "Structure of an IkappaBalpha/NF-kappaB complex.";

RL Cell 95:749-758(1998).

RR [10]

RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 73-302.

RP MEDLINE=99081292; PubMed=9865694;

RX Huxford T., Huang D.B., Malek S., Ghosh G.;

RA "The crystal structure of the IkappaBalpha/NF-kappaB complex reveals

RT mechanisms of NF-kappaB inactivation.";

RL Cell 95:759-770(1998).

CC -1- FUNCTION: INHIBITOR OF NF-KAPPA-B THAT TIGHTLY REGULATES NF-KAPPA-B

CC BE ACTIVATION BY COMPLEXING AND TRAPPING IT IN THE CYTOPLASM. MAY

CC KAPPA-B, INCLUDING CELL ADHESION, IMMUNE AND PROINFLAMMATORY

CC RESPONSES, APOPTOSIS, DIFFERENTIATION AND GROWTH. CONTROLLED BY

CC SEQUENTIAL SERINE-PHOSPHORYLATION, UBIQUITINATION AND DEGRADATION.

CC TYROSINE-PHOSPHORYLATION COULD ONLY LEAD TO DISSOCIATION FROM NF-

CC KAPPA-B.

CC -1- SUBUNIT: INTERACTS WITH P65 (RELA).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- INDUCTION: INDUCED IN ADHERENT MONOCYTES.

CC -1- PTM: PHOSPHORYLATION OF I-KAPPA-B BLOCKS ITS ABILITY TO INHIBIT

CC NF-KAPPA-B DNA-BINDING ACTIVITY.

CC -1- PTM: SUBSEQUENT TO STIMULUS-DEPENDENT PHOSPHORYLATION ON SERINES,

CC POLYUBIQUITINATION TARGETS THE PROTEIN FOR RAPID DEGRADATION VIA

CC THE UBIQUITIN SYSTEM.

CC -1- SIMILARITY: BELONGS TO THE NF-KAPPA-B INHIBITOR FAMILY.

CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.

CC -----

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CC -----

DR EMBL; M69043; AAA16489.1; -

DR EMBL; AJ249294; CAB65556.2; -

DR EMBL; AJ249295; CAB65556.2; JOINED.

DR EMBL; AJ249283; CAB65556.2; JOINED.

DR EMBL; AJ249284; CAB65556.2; JOINED.

DR EMBL; AJ249285; CAB65556.2; JOINED.

DR EMBL; AJ249286; CAB65556.2; JOINED.

DR EMBL; AY033600; AAK51149.1; -

DR EMBL; BC002601; AAH02601.1; -

DR EMBL; BC004983; AAH04983.1; -

DR PIR; A39935; A39935

DR PDB; 1NFI; 23-FEB-99.

DR PDB; 1TKN; 12-APR-99.

DR TRANSFAC; T00950; -

DR MIM; 164008; -

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 4.

PRINTS; PR01415; ANKYRIN.

SMART; SM00248; ANK; 4.

PROSITE; PS00088; ANK_REPEAT; 3.

PROSITE; PS0297; ANK_REPEAT; 1.

KW Phosphorylation; ANK repeat; Repeat; Ubiquitin conjugation;

KW 3D-structure.

FT REPEAT 73 103 ANK 1.

FT REPEAT 110 139 ANK 2.

FT REPEAT 143 172 ANK 3.

FT REPEAT 182 211 ANK 4.

FT REPEAT 216 245 ANK 5.

FT BINDING 21 21 UBIQUITIN (POTENTIAL).

FT BINDING 22 22 UBIQUITIN (POTENTIAL).

FT MOD_RES 32 32 PHOSPHORYLATION (BY IKKA AND IKKE).

FT MOD_RES 36 36 PHOSPHORYLATION (BY IKKA AND IKKE).

FT MOD_RES 42 42 PHOSPHORYLATION (BY TYR-KINASES).

FT MUTAGEN 21 21 K->R: DECREASE IN UBIQUITINATION AND

FT MUTAGEN 22 22 DEGRADATION; WHEN ASSOCIATED WITH R-22.

FT MUTAGEN 22 22 K->R: DECREASE IN UBIQUITINATION AND

FT MUTAGEN 31 31 DEGRADATION; WHEN ASSOCIATED WITH R-21.

FT MUTAGEN 32 32 D->A: LOSS OF PHOSPHORYLATION; WHEN

FT MUTAGEN 32 32 ASSOCIATED WITH A-35.

FT MUTAGEN 32 32 S->T: DECREASE IN PHOSPHORYLATION AND

FT MUTAGEN 32 32 DEGRADATION; WHEN ASSOCIATED WITH T-36.

FT MUTAGEN 35 35 S->A: LOSS OF PHOSPHORYLATION AND

FT MUTAGEN 42 42 DEGRADATION; WHEN ASSOCIATED WITH A-36.

FT MUTAGEN 234 234 D->G: NO CHANGE IN PHOSPHORYLATION.

FT MUTAGEN 262 262 Y->F: NO EFFECT.

FT MUTAGEN 263 262 S->A: NO EFFECT.

FT MUTAGEN 263 263 T->A: NO EFFECT.

SQ SEQUENCE 317 AA; 35609 MW; 088B313226786395 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 317;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHDGS 9

DB 29 RHDGS 33

RESULT 33

IKBA_CHICK STANDARD; PRT; 318 AA.

ID IKBA_CHICK

AC Q91974;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE NF-kappaB inhibitor alpha (I-kappa-B-alpha) (IkappaBalpha) (IKB-alpha)

DE (REL-associated protein pp40).

GN NFkBIA OR IKBA.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RP [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Embryonic fibroblast;

RX MEDLINE=91368196; PubMed=1891714;

RA Davis N., Ghosh S., Simmons D.L., Tempst P., Liou H.-C., Baltimore D.,

RA Bose H.R. Jr.;

RT "Rel-associated pp40: an inhibitor of the rel family of transcription

RT factors.";

RL Science 253:1268-1271(1991).

CC -1- FUNCTION: INHIBITOR OF NF-KAPPA-B THAT TIGHTLY REGULATES NF-KAPPA-B

CC ACTIVATION BY COMPLEXING AND TRAPPING IT IN THE CYTOPLASM. MAY

CC BE INVOLVED IN REGULATION OF TRANSCRIPTIONAL RESPONSES TO NF-

CC KAPPA-B, INCLUDING CELL ADHESION, IMMUNE AND PROINFLAMMATORY

CC RESPONSES, APOPTOSIS, DIFFERENTIATION AND GROWTH. CONTROLLED BY

CC SEQUENTIAL SERINE-PHOSPHORYLATION, UBIQUITINATION AND DEGRADATION.

CC TYROSINE-PHOSPHORYLATION COULD ONLY LEAD TO DISSOCIATION FROM NF-
 CC KAPPA-B (BY SIMILARITY).
 CC -|- SUBUNIT: INTERACTS WITH P65 (RELA) (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LYMPH NODE, THYMUS
 CC FOLLOWED BY LIVER, BRAIN, MUSCLE, KIDNEY, GASTROINTESTINAL AND
 CC REPRODUCTIVE TRACT.
 CC -|- PTM: SUBSEQUENT TO STIMULUS-DEPENDENT PHOSPHORYLATION ON SERINES,
 CC POLYUBIQUITINATION TARGETS THE PROTEIN FOR RAPID DEGRADATION VIA
 CC THE UBIQUITIN SYSTEM (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE NF-KAPPA-B INHIBITOR FAMILY.
 CC -|- SIMILARITY: CONTAINS 4 ANK REPEATS.
 CC -----
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 CC -----
 DR EMBL; S55765; AAB19758.1; -;
 DR EMBL; M74544; AAA49030.1; -;
 DR HSSP; P25963; IJKN.
 DR InterPro: IPR002110; ANK.
 DR Pfam; PF00023; ank; 5.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 4.
 DR PROSITE; PS0088; ANK_REPEAT; 4.
 DR PROSITE; PS0297; ANK_REPEAT; Repeat; Ubiquitin conjugation.
 KW Phosphorylation; ANK_REPEAT; Repeat; Ubiquitin conjugation.
 FT REPEAT 114 143.
 FT REPEAT 147 176 ANK 1.
 FT REPEAT 176 215 ANK 2.
 FT REPEAT 220 249 ANK 3.
 FT REPEAT 249 283 ANK 4.
 FT BINDING 21 21 UBIQUITIN (BY SIMILARITY).
 FT MOD_RES 36 36 PHOSPHORYLATION (BY IKKA AND IKKB) (BY
 FT SIMILARITY).
 FT MOD_RES 40 40 PHOSPHORYLATION (BY IKKA, IKKB AND IKKE)
 FT (BY SIMILARITY).
 FT MOD_RES 46 46 PHOSPHORYLATION (BY TYR-KINASES)
 FT (BY SIMILARITY).
 SQ SEQUENCE 318 AA; 35398 MW; 2E1BFB21B54E29F CRC64;

Query Match 41.7%; Score 5; DB 1; Length 318;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 RHDSG 9
 | | | | |
 Db 33 RHDSG 37

RESULT 34
 ID TECB_CHICK STANDARD; PRT; 329 AA.
 AC P54097;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Beta-tectorin precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ISA BROWN; TISSUE=Cochlear duct;
 RX MEDLINE=95238547; PubMed=7721949;
 RA Killick R., Legan P.K., Malenczak C., Richardson G.P.;
 RT "Molecular cloning of chick beta-tectorin, an extracellular matrix

RT molecule of the inner ear.";
 RL J. Cell Biol. 129:535-547(1995).
 CC -|- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
 CC (POTENTIAL). FOUND IN EXTRACELLULAR MATRIX.
 CC -|- TISSUE SPECIFICITY: INNER EAR (BASILAR PAPILLA, CLEAR CELLS AND
 CC LAGENA MACULA).
 CC -|- PTM: THE N-TERMINUS IS BLOCKED.
 CC -|- PTM: N-GLYCOSYLATED.
 CC -|- SIMILARITY: CONTAINS 1 ZP DOMAIN.
 CC -----
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 CC -----
 DR EMBL; L38519; AAA92461.1; -;
 DR InterPro: IPR001507; zona_pellucida.
 DR Pfam; PF00100; zona_pellucida; 1.
 DR SMART; SM0241; ZP; 1.
 DR PROSITE; PS00682; ZP_DOMAIN; 1.
 KW Extracellular matrix; Signal; Glycoprotein; GPI-anchor.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 329 BETA-TECTORIN.
 FT DOMAIN 91 283 ZP.
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 329 AA; 36899 MW; 4D66131C733C0DA2 CRC64;
 Query Match 41.7%; Score 5; DB 1; Length 329;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 HDSG 10
 | | | | |
 Db 64 HDSG 68
 RESULT 35
 ID GALT_LACCA STANDARD; PRT; 331 AA.
 AC G84905;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Galactose operon repressor.
 GN GALT.
 OS Lactobacillus casei.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1582;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=64H;
 RX MEDLINE=98268934; PubMed=9603808;
 RA Bettenbrock K., Alpert C.A.;
 RT "The gal genes for the Leloir pathway of Lactobacillus casei 64H.";
 RL Appl. Environ. Microbiol. 64:2013-2019(1998).
 CC -|- FUNCTION: REPRESSOR OF THE GALACTOSE OPERON. BINDS GALACTOSE AS AN
 CC INDUCER (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE LACI FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC -----
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OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=98053840; PubMed=9393691;
 RA Itoh Y.;
 RT "Cloning and characterization of the *aru* genes encoding enzymes of
 the catabolic arginine succinyltransferase pathway in *Pseudomonas*
 aeruginosa";
 RL J. Bacteriol. 179:7280-7290(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 Garber R.L., Gollry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 opportunistic pathogen";
 RL Nature 408:959-964(2000).
 RN [3]
 RP SEQUENCE OF 1-15.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=95010075; PubMed=7523119;
 RA Tricot C., Vander Wauven C., Wattiez R., Falmagne P., Stalon V.;
 RT "Purification and properties of a succinyltransferase from
Pseudomonas aeruginosa specific for both arginine and ornithine.";
 RL Eur. J. Biochem. 224:853-861(1994).
 CC -!- CATALYTIC ACTIVITY: Succinyl-CoA + L-arginine = CoA + N2-
 succinyl-L-arginine.
 CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
 CC -!- MISCELLANEOUS: ALSO ACTS ON L-ORNITHINE.
 CC -----
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 CC -----
 DR ENBL: AF011922; AAC46011.1; -;
 DR ENBL: AE004524; AAG04286.1; -;
 KW Arginine metabolism; Transferase; Acyltransferase; Complete proteome.
 SQ SEQUENCE 340 AA; 37245 MW; B87B6626166DD49A CRC64;

 Query Match 41.7%; Score 5; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AEFRR 6
 DB 147 AEFRR 151
 ID TP38_TREPA STANDARD; PRT; 343 AA.
 AC Q56328;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Membrane lipoprotein Tpn38(b) precursor.
 GN TPN38 OR TP0298.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLS;
 RX MEDLINE=96167817; PubMed=8598278;
 RA Stamm L.V., Hardham J.M., Frye J.G.;
 RT "Expression and sequence analysis of a *Treponema pallidum* gene,
 Tpn38(b), encoding an exported protein with homology to T. pallidum
 and *Borrelia burgdorferi* proteins.";
 RL FEMS Microbiol. Lett. 135:57-63(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLS;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
 Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 Venter J.C.;
 RT "Complete genome sequence of *Treponema pallidum*, the syphilis
 spirochete";
 RL Science 281:375-388(1998).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Probable).
 CC -!- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR ENBL: U12861; AAB02167.1; -;
 DR ENBL: AE001210; AAC65287.1; -;
 TIGR: TP0298;
 DR InterPro: IPR003760; Bmp.
 DR Pfam: PF02608; Bmp; 1.
 KW Membrane; Lipoprotein; Signal; Complete proteome.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 343 MEMBRANE LIPOPROTEIN TPN38(B).
 FT LIPID 20 20 N-ACYL DIGLYCERIDE (BY SIMILARITY).
 FT SEQUENCE 343 AA; 37881 MW; 800687C5A1420C4D CRC64;
 SQ SEQUENCE 343 AA; 37881 MW; 800687C5A1420C4D CRC64;

 Query Match 41.7%; Score 5; DB 1; Length 343;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FRHDS 8
 DB 39 FRHDS 43
 ID WTLD_BACST STANDARD; PRT; 382 AA.
 AC Q45421;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17).
 GN WTLD.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 7954;
 RX MEDLINE=96421984; PubMed=8824601;
 RA Henstra S.A., Tolner B., Hoeve Duurkens R.H., Konings W.N.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abrell J.F., Agbayani A., An H.-J., Andrews-Frankkoch C., Baldwin D.,
 Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 Flosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 Mirkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 Palazzolo M., Pittman K.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskae R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassenaar D.A., Weinstock G.M., Weissensbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.
 "The genome sequence of *Drosophila melanogaster*."
 Science 287:2185-2195(2000).
 [4]
 CHARACTERIZATION.
 STRAIN-OREGON-R;
 MEDLINE=98211586; PubMed=9551861;
 Ledent V., Gaillard F., Gautier P., Chysen A., Dambly-Chaudiere C.;
 "Expression and function of tap in the gustatory and olfactory organs
 of *Drosophila*."
 Int. J. Dev. Biol. 42:163-170(1998).
 -1- FUNCTION: MAY PLAY A ROLE IN THE SPECIFICATION OF THE SUGAR-
 SENSITIVE ADULT GUSTATORY NEURON AND AFFECT THE RESPONSE TO SUGAR
 AND SALT. REGULATED BY POXN.
 -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.

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 EMBL; AF022883; AAC80572.1; -;
 EMBL; X95845; CAA65103.1; -;
 EMBL; AE003524; AAF49352.1; -;
 FlyBase; FBgn0015550; tap.
 InterPro; IPR003015; HLH_Myc.
 InterPro; IPR001092; HLH_dlm.
 Pfam; PF00010; HLH; 1.
 SMART; SM00353; HLH; 1.
 PROSITE; PS00038; HELIX_LOOP_HELIX; FALSE_NEG.
 DNA-binding; Nuclear protein; Transcription regulation; Neurogenesis;
 Developmental protein; Differentiation.
 DNA_BIND 155 166 BASIC DOMAIN (BY SIMILARITY).
 DOMAIN 167 207 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 DOMAIN 18 23 POLY-ASP.
 DOMAIN 308 312 POLY-GLN.
 SEQUENCE 398 AA; 44850 MW; 54FF556483B18258 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 398;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYE 11
 DB 27 DSGYE 31

RESULT 42
 PNCB_BUCAI
 ID PNCB_BUCAI STANDARD; PRT; 399 AA.
 AC P57442;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
 GN PNCB OR BU361.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOKYO 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -|- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
 CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
 CC -|- PATHWAY: FIRST STEP IN PREISS-HANDLER PATHWAY LEADING TO THE
 CC SYNTHESIS OF NAD.
 CC -|- MISCELLANEOUS: REQUIRES ATP AS WELL AS PHOSPHORIBOSYL
 CC PYROPHOSPHATE FOR ACTIVITY (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE NAPRTASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AP001119; BAB13065.1; -;
 KW Transferase; Glycosyltransferase; Complete proteome.
 SQ SEQUENCE 399 AA; 46750 MW; 09A735641222EE19 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 399;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHDGS 9
 DB 282 RHDGS 286

RESULT 43
 PNCB_ECOLI
 ID PNCB_ECOLI STANDARD; PRT; 399 AA.
 AC P18133;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
 GN PNCB OR B0931.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OX Escherichia.

OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
 RC STRAIN-CEC70;
 RX MEDLINE=91009224; PubMed=2211655;
 RA Wubbolds M.G., Terpstra P., van Beilen J.B., Kingma J.,
 RA Meesters H.A.R., Witholt B.;
 RT "Variation of cofactor levels in Escherichia coli. Sequence analysis
 RT and expression of the pncB gene encoding nicotinic acid
 RT phosphoribosyltransferase.";
 RL J. Biol. Chem. 265:17665-17672(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horluchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 CC -|- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
 CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
 CC -|- PATHWAY: FIRST STEP IN PREISS-HANDLER PATHWAY LEADING TO THE
 CC SYNTHESIS OF NAD.
 CC -|- SUBCELLULAR LOCATION: Periplasmic (possible).
 CC -|- MISCELLANEOUS: REQUIRES ATP AS WELL AS PHOSPHORIBOSYL
 CC PYROPHOSPHATE FOR ACTIVITY.
 CC -|- SIMILARITY: BELONGS TO THE NAPRTASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; J05568; AAA24400.1; -;
 DR EMBL; AEG00195; AAC74017.1; -;
 DR EMBL; D90731; BAA35683.1; -;
 DR PIR; JQ0756; JQ0756.
 DR EcoGene; EGI0742; pncB.
 KW Transferase; Glycosyltransferase; Periplasmic; Complete proteome.
 FT INIT_MET 0
 SQ SEQUENCE 399 AA; 45766 MW; 37F0C0D2C3BA5C45 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 399;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHDGS 9
 DB 280 RHDGS 284

RESULT 44
 PNCB_SALTY
 ID PNCB_SALTY STANDARD; PRT; 399 AA.

Fri Sep 13 09:18:13 2002

P2253:
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
GN PNCB OR STM1004.
OS Salmonella typhimurium.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP MEDLINE=91100340; PubMed=1987148;
RA Vinitsky A., Teng H., Grubmeyer C.T.;
RT "Cloning and nucleic acid sequence of the Salmonella typhimurium pncB
gene and structure of nicotinate phosphoribosyltransferase.";
RL J. Bacteriol. 173:536-540(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
CC -1- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: FIRST STEP IN PREISS-HANDLER PATHWAY LEADING TO THE
SYNTHESIS OF NAD.
CC -1- SUBCELLULAR LOCATION: Periplasmic (possible).
CC -1- MISCELLANEOUS: REQUIRES ATP AS WELL AS PHOSPHORIBOSYL
PYROPHOSPHATE FOR ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE NAPRTASE FAMILY.
CC -----
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CC -----
DR EMBL; M55986; AAA27190.1; -;
DR EMBL; AE008743; AAL19938.1; -;
DR PIR; A39130; A39130.
DR StGene; SG10305; pncB.
KW Transferase; Glycosyltransferase; Periplasmic; Complete proteome.
FT INIT_MET 0
FT SEQUENCE 399 AA; 45530 MW; 90D9C3EDD8C092A6 CRC64;
OY 5 RHDSSG 9
Db 280 RHDSSG 284
|||||
Query Match 41.7%; Score 5; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 RHDSSG 9
Db 280 RHDSSG 284
|||||
RESULT 45
RSBP_BACSU
ID RSBP_BACSU STANDARD; PRT; 403 AA.
AC O07014;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE SigmaB regulation protein phosphatase 2C rsbp (EC 3.1.3.16).
GN RSBP.

OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Denizot F.C.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=20098692; PubMed=10632888;
RA Vijay K., Brody M.S., Fredlund E., Price C.W.;
RT "A PP2C phosphatase containing a PAS domain is required to convey
signals of energy stress to the sigmaB transcription factor of
Bacillus subtilis.";
RL Mol. Microbiol. 35:180-188(2000).
CC -1- FUNCTION: REQUIRED TO CONVEY SIGNALS OF ENERGY STRESS TO THE
SIGMAB TRANSCRIPTION FACTOR. DEPHOSPHORYLATES THE RSbv ANTI-ANTI-
SIGMA FACTOR.
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -1- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL; Z94043; CAB08010.1; -;
DR EMBL; Z99121; CAB15416.1; -;
DR Subtilist; BG12441; rsbp.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00989; PAS; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01112; PAS; 1.
KW Hydrolase; Complete proteome. PAS.
FT DOMAIN 1 42
FT SEQUENCE 403 AA; 46030 MW; 104A3651F7C7962 CRC64;
OY 5 RHDSSG 9
Db 94 RHDSSG 98
|||||
RESULT 46
SUFD_ECOLI
ID SUFD_ECOLI STANDARD; PRT; 423 AA.
AC P77689;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sufd protein.
GN SUFD OR B1681.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;

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RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Sampaio G., Seki Y., Sivasubram S., Tagami H., Takada J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP FUNCTION.
RC STRAIN=K12 / MG1655;
RX MEDLINE=99255563; PubMed=10322040;
RA Patzer S.I., Hantke K.;
RT "Sufs is a Nfs-like protein, and SufD is necessary for stability of
the 2Fe-2S Feuf protein in Escherichia coli.";
RL J. Bacteriol. 181:3307-3309(1999).
CC -!- FUNCTION: REQUIRED FOR THE STABILITY OF THE HUFP PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE UPF0051 (YCF24) FAMILY.
CC -----
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CC -----
DR EMBL; AE000263; AAC74751.1; -
DR EMBL; D90811; BAA15456.1; -
DR EMBL; D90812; BAA15462.1; -
DR EcoGene; EG13963; sufd.
DR InterPro; IPR000825; UPF0051.
DR Pfam; PF01458; UPF0051; 1.
KW Complete proteome.
SQ SEQUENCE 423 AA; 46822 MW; 5744291F1E0AE825 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
Db 104 SGYEV 108
|||||

RESULT 47
TRME_UREPA
ID TRME_UREPA STANDARD; PRT; 438 AA.
AC QPRC7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable tRNA modification GTPase trme.
GN TRME OR THDF OR U0018.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=SEROVAR 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum.";
RL Nature 407:757-762(2000).
CC -!- FUNCTION: EXHIBITS A VERY HIGH INTRINSIC GTPASE HYDROLYSIS RATE.
CC INVOLVED IN THE BIOSYNTHESIS OF THE HYPERMODIFIED NUCLEOSIDE 5-
CC METHYLAMINOMETHYL-2-THIOURIDINE, WHICH IS FOUND IN THE WOBBLE
CC POSITION OF SOME TRNAS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
CC PROTEINS. TRME SUBFAMILY.
CC -----
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CC -----
DR EMBL; AE002101; AAF30423.1; -
DR InterPro; IPR002917; MMR_HSR1.
DR InterPro; IPR001806; Ras_trnsmng.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PRINTS; PR00449; GTP-binding; Complete proteome.
KW tRNA processing; RSTRNSFRMNG.
FT NP_BIND 221 228 GTP (POTENTIAL).
FT NP_BIND 268 272 GTP (POTENTIAL).
FT NP_BIND 325 328 GTP (POTENTIAL).
SQ SEQUENCE 438 AA; 49463 MW; D83E4730D8AAC0EB CRC64;

Query Match 41.7%; Score 5; DB 1; Length 438;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEPRH 6
Db 154 AEPRH 158
|||||

RESULT 48
DPD2_CAEEL
ID DPD2_CAEEL STANDARD; PRT; 451 AA.
AC Q19366;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable DNA polymerase delta small subunit (EC 2.7.7.7).
GN FI2F6.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Kershaw J.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE FUNCTION OF THE SMALL SUBUNIT IS NOT YET CLEAR.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + [DNA](N).
CC -!- SUBUNIT: HETERODIMER WITH SUBUNITS OF 125 KDA AND 50 KDA (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE DELTA/II SMALL SUBUNIT
CC FAMILY.
CC -----
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EMBL; Z73425; CAA97785.1; -.
DR WormPep; F12F6.7; CR05595;
KW Hypothetical protein; Transferase; DNA-directed DNA polymerase;
KW DNA replication; Nuclear protein.
SQ SEQUENCE 451 AA; 50403 MW; 6DCC014A809942C6 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRR 6
| | | | |
Db 406 AEFRR 410

RESULT 49

SVC_HELPJ
ID SVC_HELPJ STANDARD; PRT; 465 AA.
AC Q9ZKW6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CysteinyI-trNA synthetase (EC 6.1.1.16) (Cysteine--trNA ligase)
DE (CysRS).
GN CYSS OR JHP0818.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999)
CC -!- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP +
CC diphosphate + L-cysteinyI-trNA(Cys).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC STRONG, TO METHIONYL-TRNA SYNTHETASE.

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EMBL; AE001511; AAD06399.1; -.
DR InterPro; IPR002308; trNA-synt_1e.
DR Pfam; PF01406; trNA-synt_1e; 1.
DR PRINTS; PR00983; trNASYNTHCYS.
DR PROSITE; PS00178; trNA-trNA_LIGASE_1; FALSE_NEG.
KW Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 29 39 "HIGH" REGION.
FT SITE 269 273 "KMSKS" REGION.
FT BINDING 272 272 ATP (BY SIMILARITY).
SQ SEQUENCE 465 AA; 53306 MW; 336AB8BAE0D4476A CRC64;

Query Match 41.7%; Score 5; DB 1; Length 465;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
| | | | |
Db 56 SGYEV 60

RESULT 50

SVC_HELPY
ID SVC_HELPY STANDARD; PRT; 465 AA.
AC P41259;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CysteinyI-trNA synthetase (EC 6.1.1.16) (Cysteine--trNA ligase)
DE (CysRS).
GN CYSS OR HP0886.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kechum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Fleischmann R.D., Ketchum K.A., Zhou L., Kirkness E.F., Peterson S.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Glodek A.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Adams M.D., Hickey E.K.,
RA McKenney K., Fitzgerald L.M., Lee N., Peterson J.D., Kelley J.M.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Wallin E.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RA "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
RN [2]
RP SEQUENCE OF 278-465 FROM N.A.
RX STRAIN=ATCC 49503 / 60190;
MEDLINE=94193753; PubMed=8144644;
RA Cover T.L., Tummuru M.K., Cao P., Thompson S.A., Blaser M.J.;
RT "Divergence of genetic sequences for the vacuolating cytotoxin among
RL Helicobacter pylori strains.";
RN J. Biol. Chem. 269:10566-10573(1994).
RN [3]
RP SEQUENCE OF 407-465 FROM N.A.
RX STRAIN=CCUG 17874 / NCTC 11638;
MEDLINE=94222514; PubMed=8188917;
RA Phadnis S.H., Silver D.J., Janzon L., Normark S., Westblom T.U.;
RT "Pathological significance and molecular characterization of the
RT vacuolating toxin gene of Helicobacter pylori.";
RL Infect. Immun. 62:1557-1565(1994).
CC -!- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP +
CC diphosphate + L-cysteinyI-trNA(Cys).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC STRONG, TO METHIONYL-TRNA SYNTHETASE.

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EMBL; AE000598; AAD07934.1; -.

DR EMBL; U05676; AAA17656.1; -;
 DR EMBL; U07145; AAA18866.1; -;
 DR PIR; C53739; C53739.
 DR TIGR; HP0886; -;
 DR InterPro; IPR002308; tRNA-synt_le.
 DR InterPro; IPR001412; tRNA-synt_I.
 DR Pfam; PF01406; tRNA-synt_le; 1.
 DR PRINTS; PR00983; TRNASYNTHCYS.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 29 39 "HIGH" REGION.
 FT SITE 269 273 "KMSKS" REGION.
 FT BINDING 272 272 ATP (BY SIMILARITY).
 FT VARIANT 280 280 V -> I (IN STRAIN ATCC 49503).
 FT VARIANT 332 332 T -> N (IN STRAIN ATCC 49503).
 FT VARIANT 392 392 I -> V (IN STRAIN ATCC 49503).
 FT VARIANT 432 432 R -> Q (IN STRAINS ATCC 49503 AND NCTC 11638).
 FT VARIANT 434 434 D -> N (IN STRAIN NCTC 11638).
 FT VARIANT 440 440 S -> H (IN STRAIN ATCC 49503).
 SQ SEQUENCE 465 AA; 53131 MW; B7053D58BCD87E30 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 465;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SGYEV 12
 Db 56 SGYEV 60

Search completed: September 13, 2002, 09:09:20
 Job time: 210 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:06:10 : Search time 26.2 Seconds
(without alignments)
79.234 Million cell updates/sec

Title: US-09-580-015-42_COPY_1_12

Perfect score: 12

Sequence: 1 DAEFRHDSGYEV 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- 1: SPTEMBL19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_virus.*
- 17: sp_bacteria.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	19	4 Q9UC8	Q9UC8 homo sapien
2	12	100.0	28	4 Q9UCD1	Q9UCD1 homo sapien
3	12	100.0	30	4 Q9UCA9	Q9UCA9 homo sapien
4	12	100.0	33	4 Q9UC33	Q9UC33 homo sapien
5	12	100.0	82	4 P78438	P78438 homo sapien
6	12	100.0	82	4 Q16014	Q16014 homo sapien
7	12	100.0	82	4 Q16019	Q16019 homo sapien
8	12	100.0	82	4 Q16020	Q16020 homo sapien
9	12	100.0	534	13 Q93296	Q93296 gallus gall
10	12	100.0	569	13 Q9PVL1	Q9PVL1 gallus gall
11	12	100.0	695	6 Q95KN7	Q95KN7 macaca fasc
12	12	100.0	695	11 Q60496	Q60496 cavia sp. p
13	12	100.0	695	13 Q9DG38	Q9DG38 gallus gall
14	12	100.0	751	13 Q9DGJ7	Q9DGJ7 gallus gall
15	12	100.0	770	6 Q9TUI0	Q9TUI0 sus scrofa
16	10	83.3	97	4 Q13778	Q13778 homo sapien

SUMMARIES

17	58.3	7	16	Q9A4N9	Q9A4N9 caulobacter
18	50.0	6	2	053951	053951 streptomyce
19	50.0	6	240	16 Q92PX4	Q92PX4 rhizobium m
20	50.0	6	265	2 Q9AQL8	Q9AQL8 pseudomonas
21	50.0	6	279	5 Q9VID7	Q9VID7 drosophila
22	50.0	6	372	5 Q95YK6	Q95YK6 ciona savig
23	50.0	6	380	17 Q30016	Q30016 archaeoglob
24	50.0	6	408	2 Q9L0L5	Q9L0L5 streptomyce
25	50.0	6	418	2 Q9KY96	Q9KY96 streptomyce
26	50.0	6	432	2 Q93RK7	Q93RK7 bacillus sp
27	50.0	6	444	10 Q941F1	Q941F1 arabidopsis
28	50.0	6	447	10 Q94340	Q94340 arabidopsis
29	50.0	6	453	17 Q30322	Q30322 archaeoglob
30	50.0	6	515	10 Q9M9Y7	Q9M9Y7 arabidopsis
31	50.0	6	533	11 Q08569	Q08569 cavia porce
32	50.0	6	576	5 Q952X3	Q952X3 caenorhabdi
33	50.0	6	642	5 Q952X4	Q952X4 caenorhabdi
34	50.0	6	699	13 Q57394	Q57394 narke japon
35	41.7	5	39	5 Q9TX98	Q9TX98 caenorhabdi
36	41.7	5	105	2 Q87879	Q87879 thauera aro
37	41.7	5	107	5 Q9W5B9	Q9W5B9 drosophila
38	41.7	5	108	12 Q9DH37	Q9DH37 turkey herp
39	41.7	5	111	2 Q9F8D1	Q9F8D1 rhizobium e
40	41.7	5	112	16 Q92629	Q92629 chlamydia p
41	41.7	5	115	10 Q94KV8	Q94KV8 brassica na
42	41.7	5	117	17 Q97Y29	Q97Y29 sulfolobus
43	41.7	5	120	12 Q9JOD7	Q9JOD7 human coxa
44	41.7	5	124	11 Q9QZV0	Q9QZV0 rattus norv
45	41.7	5	128	2 Q9EYQ6	Q9EYQ6 thermus the
46	41.7	5	130	12 Q9WRV3	Q9WRV3 human coxa
47	41.7	5	130	12 Q9WRX4	Q9WRX4 human coxa
48	41.7	5	131	12 Q9L2I0	Q9L2I0 human coxa
49	41.7	5	132	3 Q9P6S6	Q9P6S6 schizosacch
50	41.7	5	132	3 P78948	P78948 schizosacch
51	41.7	5	132	12 Q9JA98	Q9JA98 human coxa
52	41.7	5	132	12 Q9JA95	Q9JA95 human coxa
53	41.7	5	134	12 Q91LM4	Q91LM4 cetacean mo
54	41.7	5	134	12 Q912H9	Q912H9 human coxa
55	41.7	5	135	11 Q9CTV6	Q9CTV6 mus musculu
56	41.7	5	136	16 Q9A2S3	Q9A2S3 caulobacter
57	41.7	5	142	5 Q16896	Q16896 caenorhabdi
58	41.7	5	143	17 Q97Z17	Q97Z17 sulfolobus
59	41.7	5	153	4 Q9NW29	Q9NW29 homo sapien
60	41.7	5	163	5 Q917Y4	Q917Y4 drosophila
61	41.7	5	166	10 Q94KV6	Q94KV6 brassica ca
62	41.7	5	167	2 Q9S2W3	Q9S2W3 streptomyce
63	41.7	5	173	4 Q9H627	Q9H627 homo sapien
64	41.7	5	174	2 Q52573	Q52573 amycolatops
65	41.7	5	186	5 Q17303	Q17303 caenorhabdi
66	41.7	5	195	12 Q87073	Q87073 pseudorabdi
67	41.7	5	195	16 Q06241	Q06241 mycobacteri
68	41.7	5	196	16 Q97889	Q97889 mycobacteri
69	41.7	5	198	5 Q9VGB9	Q9VGB9 drosophila
70	41.7	5	199	4 Q9HBL1	Q9HBL1 homo sapien
71	41.7	5	208	5 Q62213	Q62213 caenorhabdi
72	41.7	5	209	2 Q86679	Q86679 streptomyce
73	41.7	5	219	17 Q9HQ48	Q9HQ48 halobacteri
74	41.7	5	220	16 Q9PP41	Q9PP41 campylobact
75	41.7	5	222	10 Q94AF0	Q94AF0 arabidopsis
76	41.7	5	226	16 Q9KBX0	Q9KBX0 bacillus ha
77	41.7	5	230	2 Q9F644	Q9F644 pseudomonas
78	41.7	5	231	16 Q98HL6	Q98HL6 rhizobium l
79	41.7	5	232	2 Q9ZHS1	Q9ZHS1 brucella ab
80	41.7	5	233	16 Q9FD95	Q9FD95 rhizobium m
81	41.7	5	235	4 Q96LI7	Q96LI7 homo sapien
82	41.7	5	239	5 Q9XU23	Q9XU23 caenorhabdi
83	41.7	5	246	16 Q9K850	Q9K850 bacillus ha
84	41.7	5	246	16 Q92ED0	Q92ED0 listeria in
85	41.7	5	258	2 Q93UM1	Q93UM1 synecococc
86	41.7	5	258	10 Q64690	Q64690 arabidopsis
87	41.7	5	259	2 Q9L3J3	Q9L3J3 clostridium
88	41.7	5	262	16 Q930P5	Q930P5 rhizobium m
89	41.7	5	264	5 Q95R29	Q95R29 drosophila

90	5	41.7	279	16	Q9I453 pseudomonas	163	5	41.7	399	16	Q9HUP4	Q9hup4 pseudomonas
91	5	41.7	280	5	Q9VZV7 drosophila	164	5	41.7	399	16	Q99UQ7	Q99uq7 staphylococ
92	5	41.7	280	6	Q9NOC8	165	5	41.7	401	10	Q947T5	Q947t5 oryza sativ
93	5	41.7	282	12	Q9J0D6	166	5	41.7	402	16	Q9JYM9	Q9jym9 neisseria m
94	5	41.7	283	4	Q96C87	167	5	41.7	404	16	Q929S9	Q929s9 listeria in
95	5	41.7	284	5	Q9VZV6	168	5	41.7	406	2	Q93CM9	Q93cm9 helicobacte
96	5	41.7	284	12	Q9YLM5	169	5	41.7	408	10	Q9FFN2	Q9ffn2 arabidopsis
97	5	41.7	286	4	Q96MH2	170	5	41.7	412	5	Q960J5	Q960j5 drosophila
98	5	41.7	286	17	Q97UJ5	171	5	41.7	419	16	Q9JTM8	Q9jtm8 neisseria m
99	5	41.7	288	3	Q9P3H2	172	5	41.7	422	2	Q9L9K7	Q9l9k7 pasteurella
100	5	41.7	288	10	Q9XII9	173	5	41.7	431	2	Q54883	Q54883 streptococ
101	5	41.7	292	13	Q9I0C3	174	5	41.7	432	4	Q9UJL9	Q9ujl9 homo sapien
102	5	41.7	294	11	Q9D6T2	175	5	41.7	432	17	O27470	O27470 methanother
103	5	41.7	294	11	Q9D6S3	176	5	41.7	433	3	Q94415	Q94415 schizosacch
104	5	41.7	294	16	P740I1	177	5	41.7	435	16	O25942	O25942 helicobacte
105	5	41.7	303	11	Q9D6Y2	178	5	41.7	435	16	Q9KN67	Q9kn67 vibrio chol
106	5	41.7	304	3	Q12688	179	5	41.7	439	17	O26959	O26959 methanother
107	5	41.7	304	17	Q9HQM4	180	5	41.7	441	16	Q9KSB1	Q9ksb1 vibrio chol
108	5	41.7	307	16	Q97QE2	181	5	41.7	442	10	O49878	O49878 lyopersico
109	5	41.7	308	2	Q60226	182	5	41.7	443	16	Q9RYV3	Q9ryv3 drosophila
110	5	41.7	308	5	Q23078	183	5	41.7	444	5	O9W5X8	O9w5x8 drosophila
111	5	41.7	310	2	Q9L4N6	184	5	41.7	452	17	Q9HQO2	Q9hqo2 halobacteri
112	5	41.7	310	13	Q9L168	185	5	41.7	453	5	O96420	O96420 drosophila
113	5	41.7	310	16	Q92R59	186	5	41.7	453	5	Q9W438	Q9w438 drosophila
114	5	41.7	312	2	O69355	187	5	41.7	453	10	Q9FYU2	Q9fyu2 cucumis sat
115	5	41.7	313	13	Q9PU78	188	5	41.7	456	5	O9VRX6	O9vrx6 drosophila
116	5	41.7	315	5	Q9N4G5	189	5	41.7	456	10	O92PW6	O92pw6 arabidopsis
117	5	41.7	317	2	P72260	190	5	41.7	456	10	Q9C8Y7	Q9c8y7 arabidopsis
118	5	41.7	317	2	Q53126	191	5	41.7	460	16	Q9Z6P6	Q9z6p6 chlamydia p
119	5	41.7	318	2	Q9AD28	192	5	41.7	462	2	O9KXV1	O9kxv1 streptomyce
120	5	41.7	323	16	Q9KC88	193	5	41.7	463	2	O85871	O85871 sphingomona
121	5	41.7	325	2	Q9F8A4	194	5	41.7	463	10	O9MLW3	Q9mlw3 arabidopsis
122	5	41.7	325	2	Q9FAA4	195	5	41.7	463	16	O07599	O07599 bacillus su
123	5	41.7	327	13	Q9I914	196	5	41.7	464	2	Q9AI65	Q9ai65 erwinia rha
124	5	41.7	328	13	Q9I1878	197	5	41.7	464	17	Q9UXN4	Q9uxn4 sulfolobus
125	5	41.7	328	13	Q9I1893	198	5	41.7	467	5	Q9U2S1	Q9u2s1 caenorhabdi
126	5	41.7	330	17	Q9HI47	199	5	41.7	474	4	O9H751	Q9h751 homo sapien
127	5	41.7	330	17	Q97729	200	5	41.7	474	4	Q9HC44	Q9hc44 homo sapien
128	5	41.7	332	11	Q9WVN8	201	5	41.7	480	2	O34442	Q34442 serratia ma
129	5	41.7	336	15	Q98YA3	202	5	41.7	481	10	Q9SV17	Q9sv17 arabidopsis
130	5	41.7	337	10	Q9LWU5	203	5	41.7	481	10	Q9I1H5	Q9i1h5 pseudomonas
131	5	41.7	337	11	Q9CSD1	204	5	41.7	486	16	O9W251	Q9w251 thermotoga
132	5	41.7	338	10	Q9XHX8	205	5	41.7	489	4	Q96K22	Q96k22 homo sapien
133	5	41.7	340	10	Q9M2N4	206	5	41.7	491	11	Q9JRM0	Q9jrm0 mus musculu
134	5	41.7	340	10	Q9FX73	207	5	41.7	503	16	Q9CDJ9	Q9cdj9 lactococcus
135	5	41.7	342	16	Q9A5C3	208	5	41.7	506	12	O66415	O66415 dolphin mor
136	5	41.7	342	16	Q9A5C3	209	5	41.7	507	5	Q27694	Q27694 musca domes
137	5	41.7	345	4	Q9NPU7	210	5	41.7	509	16	P72957	P72957 synechocyst
138	5	41.7	346	4	Q9NFB6	211	5	41.7	516	12	Q9IW00	Q9iw00 pseudorabie
139	5	41.7	346	5	Q17980	212	5	41.7	518	6	Q9MYI8	Q9myi8 oryctolagus
140	5	41.7	346	11	Q9Z101	213	5	41.7	530	17	Q97329	Q97329 sulfolobus
141	5	41.7	350	13	Q902R7	214	5	41.7	531	17	Q97V62	Q97v62 sulfolobus
142	5	41.7	350	16	Q92FN6	215	5	41.7	549	5	O9V6S5	Q9v6s5 drosophila
143	5	41.7	351	5	O97111	216	5	41.7	555	12	O9IHR4	Q9ihr4 pseudorabie
144	5	41.7	351	16	Q9AT9	217	5	41.7	558	12	O91HR5	P91342 caenorhabdi
145	5	41.7	353	16	Q98CD4	218	5	41.7	560	5	P91342	Q9g3f7 pseudorabie
146	5	41.7	358	16	Q9K7X7	219	5	41.7	577	12	O9Q3F7	O9qyc0 pseudorabie
147	5	41.7	368	16	Q98NF6	220	5	41.7	580	4	Q9H0W3	Q9h0w3 homo sapien
148	5	41.7	372	16	Q92TE5	221	5	41.7	582	10	Q94HB7	Q94hb7 oryza sativ
149	5	41.7	374	11	Q9FTK9	222	5	41.7	591	10	Q941X9	Q941x9 oryza sativ
150	5	41.7	374	11	Q9L1Y2	223	5	41.7	591	10	Q90282	Q90282 croctalus at
151	5	41.7	383	13	O9QXD3	224	5	41.7	609	13	Q90282	Q9dbn9 mus musculu
152	5	41.7	385	10	O39611	225	5	41.7	619	11	Q9DBN9	O92c63 listeria in
153	5	41.7	386	16	Q9PN80	226	5	41.7	620	16	Q92C63	O04086 arabidopsis
154	5	41.7	392	3	Q13491	227	5	41.7	625	10	O04086	O76144 neospora ca
155	5	41.7	392	16	Q97DG9	228	5	41.7	626	5	O76144	Q9p604 neurospora
156	5	41.7	393	17	O57920	229	5	41.7	631	3	Q9PF04	Q9pqp3 mycoplasma
157	5	41.7	393	17	O57920	230	5	41.7	635	16	O98QP3	O60624 homo sapien
158	5	41.7	394	2	Q9KY56	231	5	41.7	636	4	O60624	O11424 duck adenov
159	5	41.7	394	16	Q9PED1	232	5	41.7	644	12	O11424	P87656 duck adenov
160	5	41.7	395	16	O9PDQ5	233	5	41.7	644	12	P87656	O97132 drosophila
161	5	41.7	396	10	Q94K49	234	5	41.7	646	5	O97132	
162	5	41.7	398	16	Q9HW26	235	5	41.7				

236	5	41.7	652	2	Q9S6N9	Q9S6N9 bacillus th	309	5	41.7	1719	11	P97789	P97789 mus musculus
237	5	41.7	655	2	Q9ZB16	Q9ZB16 streptomyc	310	5	41.7	1729	3	Q10287	Q10287 schizosacch
238	5	41.7	657	10	Q94C06	Q94C06 ipomoea bat	311	5	41.7	1767	5	Q9W4F5	Q9W4F5 drosophila
239	5	41.7	660	5	Q19907	Q19907 caenorhabdi	312	5	41.7	1767	5	Q24495	Q24495 drosophila
240	5	41.7	663	5	Q3VLG3	Q9Vlg3 drosophila	313	5	41.7	1791	10	Q9L0M0	Q9L0M0 arabidopsis
241	5	41.7	666	4	Q96EW6	Q96ew6 homo sapien	314	5	41.7	1908	4	Q9UF08	Q9uf08 homo sapien
242	5	41.7	687	16	Q9ABL3	Q9abl3 caulobacter	315	5	41.7	1963	5	Q9VSK5	Q9vsk5 drosophila
243	5	41.7	697	4	Q60339	Q60339 homo sapien	316	5	41.7	1966	5	Q9NHX6	Q9nhx6 drosophila
244	5	41.7	704	13	Q90865	Q90865 gallus gall	317	5	41.7	2127	12	Q57294	Q57294 rabies viru
245	5	41.7	706	16	Q9KPP7	Q9kpp7 vibrio chol	318	5	41.7	2127	12	Q9JH63	Q9jh63 rabies viru
246	5	41.7	708	16	Q9CP32	Q9cp32 pasteurella	319	5	41.7	2127	12	Q9JPJ5	Q9ipj5 rabies viru
247	5	41.7	712	11	Q99K94	Q99k94 mus musculu	320	5	41.7	2187	12	Q9QSN9	Q9qsn9 human coxa
248	5	41.7	718	16	Q9PQK8	Q9pqk8 ureaplasma	321	5	41.7	2187	12	Q9YLGS	Q9ylgs human coxa
249	5	41.7	719	2	Q9L5T4	Q9l5t4 salmonella	322	5	41.7	2440	5	Q9GP97	Q9gp97 caenorhabdi
250	5	41.7	738	5	Q9W366	Q9w366 drosophila	323	5	41.7	2872	11	Q9WUH8	Q9wuh8 rattus norv
251	5	41.7	738	5	Q15646	Q15646 dictyosteli	324	5	41.7	3291	12	Q66225	Q66225 cryptoneutr
252	5	41.7	742	10	Q94LV3	Q94lv3 oryza sativ	325	5	41.7	3857	11	Q88840	Q88840 mus musculu
253	5	41.7	745	6	Q9B8E2	Q9be82 macaca fasc	326	5	41.7	4472	5	Q9VPG0	Q9vpg0 drosophila
254	5	41.7	749	11	Q9D323	Q9d323 mus musculu	327	5	41.7	4572	10	Q40712	Q40712 oryza sativ
255	5	41.7	749	11	Q9QXK0	Q9qxxk0 rattus norv	328	5	41.7	5636	5	Q9N9M2	Q9n9m2 leishmania
256	5	41.7	749	13	Q9XGE8	Q9yge8 oncorhynch	329	4	33.3	20	2	Q93JT4	Q93jt4 pseudomonas
257	5	41.7	749	13	Q93598	Q93598 brachydanio	330	4	33.3	20	6	Q9TRA4	Q9tra4 sus scrofa
258	5	41.7	754	13	Q13131	Q13131 oncorhynch	331	4	33.3	25	2	Q9RBS9	Q9rbs9 pseudomonas
259	5	41.7	754	13	Q13132	Q13132 oncorhynch	332	4	33.3	28	2	Q9RBS7	Q9rbs7 pseudomonas
260	5	41.7	756	2	Q9ADH2	Q9adh2 streptomyc	333	4	33.3	30	11	Q9QV42	Q9qv42 rattus sp.
261	5	41.7	758	13	Q90Y17	Q90y17 tetraodon f	334	4	33.3	31	16	Q9PH62	Q9ph62 xylella fas
262	5	41.7	758	16	Q9I2M9	Q9i2m9 pseudomonas	335	4	33.3	32	2	Q9RLC0	Q9rlc0 ralstonia e
263	5	41.7	763	3	Q12653	Q12653 pichia caps	336	4	33.3	33	4	Q9HLC0	Q9hlc0 homo sapien
264	5	41.7	774	16	Q92CV7	Q92cv7 listeria in	337	4	33.3	35	2	Q9RBS5	Q9rbs5 pseudomonas
265	5	41.7	775	10	Q9A4I4	Q9a4i4 arabidopsis	338	4	33.3	40	12	Q9QN30	Q9qn30 hepatitis c
266	5	41.7	786	10	Q49888	Q49888 lycopersico	339	4	33.3	40	12	Q9QN28	Q9qn28 hepatitis c
267	5	41.7	802	5	Q9Y135	Q9y135 drosophila	340	4	33.3	40	12	Q9QN22	Q9qn22 hepatitis c
268	5	41.7	816	16	Q98HH9	Q98hh9 rhizobium l	341	4	33.3	40	12	Q9QN21	Q9qn21 hepatitis c
269	5	41.7	820	10	Q9LIE7	Q9lie7 arabidopsis	342	4	33.3	40	12	Q9QN20	Q9qn20 hepatitis c
270	5	41.7	822	16	Q9AAI3	Q9aa13 caulobacter	343	4	33.3	40	12	Q9QN19	Q9qn19 hepatitis c
271	5	41.7	843	5	Q02264	Q02264 caenorhabdi	344	4	33.3	40	12	Q9QN14	Q9qn14 hepatitis c
272	5	41.7	869	16	Q9I2V5	Q9i2v5 pseudomonas	345	4	33.3	40	12	Q9E2H4	Q9e2h4 hepatitis c
273	5	41.7	873	2	Q9I960	Q9i960 moraxella c	346	4	33.3	40	12	Q9E2H3	Q9e2h3 hepatitis c
274	5	41.7	896	10	Q96573	Q96573 lycopersico	347	4	33.3	43	2	Q9EXI6	Q9exi6 klebsiella
275	5	41.7	896	10	Q24370	Q24370 solanum tub	348	4	33.3	43	2	Q9UDJ8	Q9udj8 homo sapien
276	5	41.7	911	6	Q9TTF9	Q9ttf9 tonatia bid	349	4	33.3	46	2	Q47324	Q47324 escherichia
277	5	41.7	950	5	Q9VE45	Q9ve45 drosophila	350	4	33.3	46	12	Q991G3	Q991g3 hepatitis c
278	5	41.7	963	10	Q9T0F6	Q9t0f6 arabidopsis	351	4	33.3	46	12	Q991G2	Q991g2 hepatitis c
279	5	41.7	1007	5	Q91448	Q91448 caenorhabdi	352	4	33.3	46	12	Q991G1	Q991g1 hepatitis c
280	5	41.7	1019	5	Q961G7	Q961g7 drosophila	353	4	33.3	46	12	Q991G0	Q991g0 hepatitis c
281	5	41.7	1019	5	Q961G7	Q961g7 drosophila	354	4	33.3	46	12	Q991F9	Q991f9 hepatitis c
282	5	41.7	1032	11	Q93JG3	Q93jg3 mus musculu	355	4	33.3	46	12	Q991F8	Q991f8 hepatitis c
283	5	41.7	1046	5	Q44316	Q44316 drosophila	356	4	33.3	46	12	Q991F7	Q991f7 hepatitis c
284	5	41.7	1050	3	Q12494	Q12494 saccharomyc	357	4	33.3	46	12	Q991F6	Q991f6 hepatitis c
285	5	41.7	1090	10	Q94LC8	Q94lc8 oryza sativ	358	4	33.3	46	12	Q991F5	Q991f5 hepatitis c
286	5	41.7	1095	11	Q60784	Q60784 mus musculu	359	4	33.3	46	12	Q991F4	Q991f4 hepatitis c
287	5	41.7	1108	10	Q94ED6	Q94ed6 oryza sativ	360	4	33.3	46	12	Q991F3	Q991f3 hepatitis c
288	5	41.7	1114	5	Q9VEX0	Q9vex0 drosophila	361	4	33.3	46	12	Q991F2	Q991f2 hepatitis c
289	5	41.7	1122	10	Q22267	Q22267 arabidopsis	362	4	33.3	46	12	Q991E7	Q991e7 hepatitis c
290	5	41.7	1135	2	Q9ULI6	Q9uli6 streptomyc	363	4	33.3	46	12	Q991D8	Q991d8 hepatitis c
291	5	41.7	1182	5	Q9U7F0	Q9u7f0 spirochaet	364	4	33.3	46	12	Q991D5	Q991d5 hepatitis c
292	5	41.7	1187	10	Q9FH84	Q9fh84 arabidopsis	365	4	33.3	46	12	Q991D4	Q991d4 hepatitis c
293	5	41.7	1208	4	Q9HCF8	Q9hcf8 homo sapien	366	4	33.3	46	12	Q991D3	Q991d3 hepatitis c
294	5	41.7	1226	4	Q9NZB5	Q9nzb5 homo sapien	367	4	33.3	46	12	Q991D2	Q991d2 hepatitis c
295	5	41.7	1228	11	Q9JKB5	Q9jkb5 rattus norv	368	4	33.3	46	12	Q991D0	Q991d0 hepatitis c
296	5	41.7	1236	5	Q9VUJ2	Q9vuj2 drosophila	369	4	33.3	46	12	Q991B8	Q991b8 hepatitis c
297	5	41.7	1238	2	Q69947	Q69947 streptomyc	370	4	33.3	46	12	Q991B6	Q991b6 hepatitis c
298	5	41.7	1292	5	Q22240	Q22240 caenorhabdi	371	4	33.3	46	12	Q991B4	Q991b4 hepatitis c
299	5	41.7	1328	5	Q21043	Q21043 caenorhabdi	372	4	33.3	46	12	Q991B3	Q991b3 hepatitis c
300	5	41.7	1341	3	Q08281	Q08281 saccharomyc	373	4	33.3	46	12	Q991A9	Q991a9 hepatitis c
301	5	41.7	1342	3	Q92271	Q92271 saccharomyc	374	4	33.3	46	12	Q991A7	Q991a7 hepatitis c
302	5	41.7	1349	5	Q9NHES	Q9nhes drosophila	375	4	33.3	46	12	Q991A5	Q991a5 hepatitis c
303	5	41.7	1454	4	Q9UPS3	Q9ups3 homo sapien	376	4	33.3	46	12	Q991A1	Q991a1 hepatitis c
304	5	41.7	1480	4	Q96Q04	Q96q04 homo sapien	377	4	33.3	46	12	Q991A0	Q991a0 hepatitis c
305	5	41.7	1484	11	P70098	P70098 cricetus	378	4	33.3	46	12	Q990Z9	Q990z9 hepatitis c
306	5	41.7	1519	5	Q9W5K6	Q9w5k6 drosophila	379	4	33.3	46	12	Q990Z8	Q990z8 hepatitis c
307	5	41.7	1640	3	Q13423	Q13423 candida alb	380	4	33.3	46	12	Q990Z5	Q990z5 hepatitis c
308	5	41.7	1687	11	Q35651	Q35651 mus musculu	381	4	33.3	46	12		
			1706	11	P97790	P97790 mus musculu							

528	4	33.3	77	12	O37014	O37014 newcastile d	601	4	33.3	88	2	O48224	O48224 haemophilus
529	4	33.3	77	12	O37349	O37349 newcastile d	602	4	33.3	88	2	O68743	O68743 versinia pe
530	4	33.3	77	12	O83774	O83774 newcastile d	603	4	33.3	88	10	O49916	O49916 picea abies
531	4	33.3	77	12	O83776	O83776 newcastile d	604	4	33.3	88	10	O49917	O49917 picea abies
532	4	33.3	77	12	O83778	O83778 newcastile d	605	4	33.3	88	10	O49918	O49918 picea abies
533	4	33.3	77	12	O83784	O83784 newcastile d	606	4	33.3	88	12	O91F56	O91F56 human enter
534	4	33.3	77	12	O83786	O83786 newcastile d	607	4	33.3	88	16	O97GC4	O97GC4 clostridium
535	4	33.3	77	12	O83788	O83788 newcastile d	608	4	33.3	89	6	O9TS76	O9TS76 bos taurus
536	4	33.3	77	12	O83790	O83790 newcastile d	609	4	33.3	89	6	O9MYR4	O9MYR4 bos indicus
537	4	33.3	77	12	O83792	O83792 newcastile d	610	4	33.3	89	7	O19492	O19492 gallus gall
538	4	33.3	77	12	O83796	O83796 newcastile d	611	4	33.3	89	7	O19500	O19500 gallus gall
539	4	33.3	77	12	O83798	O83798 newcastile d	612	4	33.3	89	7	O62863	O62863 gallus gall
540	4	33.3	77	12	O83800	O83800 newcastile d	613	4	33.3	89	12	O91F57	O91F57 human enter
541	4	33.3	77	12	O83802	O83802 newcastile d	614	4	33.3	89	12	O99226	O99226 non-a non-b
542	4	33.3	77	12	O83804	O83804 newcastile d	615	4	33.3	89	16	O9KUX5	O9KUX5 vibrio chol
543	4	33.3	77	12	O83806	O83806 newcastile d	616	4	33.3	90	2	O54206	O54206 streptomyce
544	4	33.3	77	12	O83810	O83810 newcastile d	617	4	33.3	90	2	O93D08	O93D08 unidentified
545	4	33.3	77	12	O83812	O83812 newcastile d	618	4	33.3	90	5	O9NLG9	O9NLG9 leishmania
546	4	33.3	77	12	O83814	O83814 newcastile d	619	4	33.3	90	5	O95TF2	O95TF2 drosophila
547	4	33.3	77	12	O83818	O83818 newcastile d	620	4	33.3	90	8	O9TAE5	O9TAE5 acorus cala
548	4	33.3	77	12	O83822	O83822 newcastile d	621	4	33.3	91	2	O9L5F8	O9L5F8 salmonella
549	4	33.3	77	12	O83824	O83824 newcastile d	622	4	33.3	91	3	O00065	O00065 ashbya goss
550	4	33.3	77	12	O83826	O83826 newcastile d	623	4	33.3	91	3	O9U6Z1	O9U6Z1 trypanosoma
551	4	33.3	77	12	O83828	O83828 newcastile d	624	4	33.3	91	5	O19566	O19566 caenorhabdi
552	4	33.3	77	12	O83830	O83830 newcastile d	625	4	33.3	91	8	O92X15	O92X15 isoetes lac
553	4	33.3	77	12	O83832	O83832 newcastile d	626	4	33.3	91	8	O9WU04	O9WU04 mus musculu
554	4	33.3	77	12	O83834	O83834 newcastile d	627	4	33.3	91	12	O91F55	O91F55 human enter
555	4	33.3	77	12	O83836	O83836 newcastile d	628	4	33.3	92	2	O9KJF5	O9KJF5 thauera aro
556	4	33.3	77	12	O83838	O83838 newcastile d	629	4	33.3	92	2	O935M7	O935M7 salmonella
557	4	33.3	77	12	O83840	O83840 newcastile d	630	4	33.3	92	5	O26773	O26773 trypanosoma
558	4	33.3	77	12	O83842	O83842 newcastile d	631	4	33.3	92	8	O21435	O21435 trypanosoma
559	4	33.3	77	12	O83844	O83844 newcastile d	632	4	33.3	92	10	O9AT01	O9AT01 phytophthor
560	4	33.3	77	12	O83846	O83846 newcastile d	633	4	33.3	92	16	O9HWW8	O9HWW8 pseudomonas
561	4	33.3	77	12	O83848	O83848 newcastile d	634	4	33.3	93	3	O96TV8	O96TV8 pleurotus o
562	4	33.3	77	12	O83850	O83850 newcastile d	635	4	33.3	94	2	O923Y2	O923Y2 pseudomonas
563	4	33.3	77	12	O83852	O83852 newcastile d	636	4	33.3	94	5	O9XWC0	O9XWC0 caenorhabdi
564	4	33.3	77	12	O83854	O83854 newcastile d	637	4	33.3	94	5	P81260	P81260 plasmodium
565	4	33.3	77	12	O83856	O83856 newcastile d	638	4	33.3	94	6	O9N0N2	O9N0N2 sus scrofa
566	4	33.3	77	12	O83858	O83858 newcastile d	639	4	33.3	94	10	O9LNE5	O9LNE5 arabidopsis
567	4	33.3	77	12	O83860	O83860 newcastile d	640	4	33.3	94	16	P72681	P72681 synecocyst
568	4	33.3	77	12	O83862	O83862 newcastile d	641	4	33.3	94	16	O91740	O91740 pseudomonas
569	4	33.3	77	12	O83864	O83864 newcastile d	642	4	33.3	95	2	O9EW18	O9EW18 streptococc
570	4	33.3	77	12	O83866	O83866 newcastile d	643	4	33.3	95	5	O94751	O94751 schistosoma
571	4	33.3	77	12	O83868	O83868 newcastile d	644	4	33.3	95	12	O98470	O98470 tacaribe vi
572	4	33.3	77	12	O83870	O83870 newcastile d	645	4	33.3	96	5	O9VTD0	O9VTD0 drosophila
573	4	33.3	77	12	O83872	O83872 newcastile d	646	4	33.3	96	8	O79363	O79363 lamprothamn
574	4	33.3	77	12	O83874	O83874 newcastile d	647	4	33.3	96	8	O79314	O79314 chara coral
575	4	33.3	77	12	O83876	O83876 newcastile d	648	4	33.3	96	8	O79307	O79307 asplenium n
576	4	33.3	77	12	O83878	O83878 newcastile d	649	4	33.3	96	9	O78743	O78743 anthoceros
577	4	33.3	77	12	O83880	O83880 newcastile d	650	4	33.3	96	11	O88025	O88025 bacterioph
578	4	33.3	77	12	O83882	O83882 newcastile d	651	4	33.3	96	11	O88518	O88518 mus musculu
579	4	33.3	77	12	O83884	O83884 newcastile d	652	4	33.3	97	2	O9ANM4	O9ANM4 bradyrhizob
580	4	33.3	77	12	O83886	O83886 newcastile d	653	4	33.3	97	4	O9BX31	O9BX31 homo sapien
581	4	33.3	77	12	O83888	O83888 newcastile d	654	4	33.3	97	5	O22645	O22645 caenorhabdi
582	4	33.3	77	12	O83890	O83890 newcastile d	655	4	33.3	97	9	O9MCT7	O9MCT7 bacterioph
583	4	33.3	77	12	O83892	O83892 newcastile d	656	4	33.3	97	9	O9MCR1	O9MCR1 bacterioph
584	4	33.3	77	12	O83894	O83894 newcastile d	657	4	33.3	97	10	O9SKR3	O9SKR3 arabidopsis
585	4	33.3	77	12	O83896	O83896 newcastile d	658	4	33.3	97	16	O9PEF4	O9PEF4 xylella fas
586	4	33.3	77	12	O83898	O83898 newcastile d	659	4	33.3	97	16	O9HY51	O9HY51 pseudomonas
587	4	33.3	77	12	O83900	O83900 newcastile d	660	4	33.3	98	2	O99Q37	O99Q37 streptomyce
588	4	33.3	77	12	O83902	O83902 newcastile d	661	4	33.3	98	2	O9X9L6	O9X9L6 salmonella
589	4	33.3	77	12	O83904	O83904 newcastile d	662	4	33.3	98	9	O9AZ31	O9AZ31 bacterioph
590	4	33.3	77	12	O83906	O83906 newcastile d	663	4	33.3	98	10	O9S9F8	O9S9F8 phytophthor
591	4	33.3	77	12	O83908	O83908 newcastile d	664	4	33.3	98	10	O9S879	O9S879 phytophthor
592	4	33.3	77	12	O83910	O83910 newcastile d	665	4	33.3	98	10	O96731	O96731 phytophthor
593	4	33.3	77	12	O83912	O83912 newcastile d	666	4	33.3	98	10	O96733	O96733 phytophthor
594	4	33.3	77	12	O83914	O83914 newcastile d	667	4	33.3	98	16	O9PBR6	O9PBR6 xylella fas
595	4	33.3	77	12	O83916	O83916 newcastile d	668	4	33.3	98	16	O927P5	O927P5 listeria in
596	4	33.3	77	12	O83918	O83918 newcastile d	669	4	33.3	99	5	O9SR20	O9SR20 drosophila
597	4	33.3	77	12	O83920	O83920 newcastile d	670	4	33.3	99	16	O97NU7	O97NU7 streptococc
598	4	33.3	77	12	O83922	O83922 newcastile d	671	4	33.3	100	2	O82901	O82901 escherichia
599	4	33.3	77	12	O83924	O83924 newcastile d	672	4	33.3	100	12	O91LA4	O91LA4 white spot
600	4	33.3	77	12	O83926	O83926 newcastile d	673	4	33.3	101	3	O96U65	O96U65 neurospora

674	4	33.3	101	10	Q9MB78	Q9mb78 nepenthes a	747	116	2	P967833	P967833 haemophilus
675	4	33.3	101	10	Q9ZPV3	Q9zpv3 arabidopsis	748	116	16	Q33365	Q33365 mycobacteri
676	4	33.3	101	17	Q9UY66	Q9uy66 pyrococcus	749	116	16	Q99TR4	Q99TR4 staphylococ
677	4	33.3	102	2	P96785	P96785 haemophilus	750	116	16	Q92R98	Q92R98 rhizobium m
678	4	33.3	102	5	Q95UJ6	Q95uj6 trypanosoma	751	116	17	Q9YGO7	Q9ygo7 aeropyrum p
679	4	33.3	103	2	O84895	O84895 salmonella	752	117	2	Q9Z542	Q9z542 streptomyce
680	4	33.3	103	2	P96784	P96784 haemophilus	753	117	3	Q9PM86	Q9pm86 emerice
681	4	33.3	103	16	Q927L8	Q927l8 listeria in	754	117	10	Q9M3N4	Q9m3n4 hordeum vul
682	4	33.3	104	9	Q9B054	Q9b054 mycobacteri	755	117	16	Q91OH1	Q91oh1 pseudomonas
683	4	33.3	104	16	Q9KR42	Q9kr42 vibrio chol	756	117	17	Q97UX4	Q97ux4 sulfolobus
684	4	33.3	105	2	P96780	P96780 haemophilus	757	117	17	Q91905	Q91905 pseudomonas
685	4	33.3	105	3	O13706	O13706 schizosacch	758	118	2	Q51978	Q51978 pseudomonas
686	4	33.3	105	8	P92542	P92542 arabidopsis	759	118	2	Q9KIH5	Q9kih5 rhizobium e
687	4	33.3	105	10	Q9T0J3	Q9t0j3 arabidopsis	760	118	4	Q92775	Q92775 homo sapien
688	4	33.3	105	10	Q9LLJ9	Q9llj9 pyrus pyrif	761	118	5	Q9VQZ5	Q9vqz5 drosophila
689	4	33.3	105	16	Q9I4T6	Q9i4t6 pseudomonas	762	118	10	Q97OM7	Q97om7 phytophthor
690	4	33.3	105	16	Q92G05	Q92g05 rickettsia	763	118	10	Q97360	Q97360 phytophthor
691	4	33.3	106	4	Q9UF02	Q9urfd2 homo sapien	764	118	10	Q91GF7	Q91gf7 oryza sativ
692	4	33.3	106	16	Q927X1	Q927x1 chlamydia p	765	118	10	Q944W0	Q944w0 phytophtho
693	4	33.3	106	17	Q97A06	Q97aq6 thermoplas	766	118	11	Q9ER36	Q9er36 mus musculu
694	4	33.3	107	16	Q9KXC6	Q9kcx6 bacillus ha	767	118	12	Q9QIZ5	Q9qiz5 faba bean n
695	4	33.3	108	5	Q9W5E1	Q9w5el drosophila	768	118	16	Q97JY6	Q97jy6 clostridium
696	4	33.3	108	17	Q9HRQ3	Q9hrq3 halobacteri	769	118	16	Q99W56	Q99w56 staphylococ
697	4	33.3	109	5	Q9V389	Q9v389 drosophila	770	119	2	Q9LCA8	Q9lca8 rhodocyc
698	4	33.3	109	11	Q9D4J0	Q9d4j0 mus musculu	771	119	2	Q9RN88	Q9rn88 salmonella
699	4	33.3	109	11	Q61064	Q61064 mus musculu	772	119	2	Q9RCE0	Q9rce0 xanthomonas
700	4	33.3	109	16	Q9HTX8	Q9htx8 pseudomonas	773	119	5	Q9W5C9	Q9w5c9 drosophila
701	4	33.3	109	16	Q92HB2	Q92hb2 rickettsia	774	119	5	Q96Z13	Q96z13 plasmodium
702	4	33.3	110	9	Q9ZWZ9	Q9zww9 mycobacteri	775	119	5	Q95YG4	Q95yg4 caenorhabdi
703	4	33.3	110	16	Q9A6S4	Q9a6s4 caulobacter	776	119	10	Q42032	Q42032 arabidopsis
704	4	33.3	111	2	Q9RIH2	Q9rih2 xenorhabdus	777	119	10	Q48571	Q48571 antirrhinum
705	4	33.3	111	5	Q9WXW1	Q9wxw1 caenorhabdi	778	119	10	Q48571	Q48571 oryza sativ
706	4	33.3	111	17	Q976V1	Q976v1 sulfolobus	779	119	10	Q94LV5	Q94lv5 neisseria m
707	4	33.3	112	2	P96777	P96777 haemophilus	780	119	16	Q9K076	Q9k076 clostridium
708	4	33.3	112	2	P96781	P96781 haemophilus	781	119	16	Q97CV8	Q97cv8 vibrio chol
709	4	33.3	112	5	Q9VJ74	Q9vj74 drosophila	782	120	2	Q9LAL3	Q9lal3 moraxella c
710	4	33.3	113	3	Q9HEU4	Q9heu4 giberella	783	120	2	Q93RN6	Q93rn6 xenorhabdus
711	4	33.3	113	4	Q96QI2	Q96qi2 homo sapien	784	120	4	O75408	O75408 homo sapien
712	4	33.3	113	10	Q9M3N2	Q9m3n2 vicia faba	785	120	16	Q986B6	Q986b6 rhizobium l
713	4	33.3	113	11	Q9CTA1	Q9ctal mus musculu	786	120	16	Q97NU5	Q97nu5 streptococ
714	4	33.3	113	12	Q86533	Q86533 hepatitis a	787	120	17	Q9YCU9	Q9ycu9 aeropyrum p
715	4	33.3	113	12	Q9IX52	Q9ix52 human enter	788	120	17	Q9XAS9	Q9xas9 rhodobacter
716	4	33.3	113	12	Q9IX51	Q9ix51 human enter	789	121	2	P96782	P96782 haemophilus
717	4	33.3	113	12	Q9IX50	Q9ix50 human enter	790	121	2	P96782	P96782 haemophilus
718	4	33.3	113	12	Q9IX49	Q9ix49 human enter	791	121	4	Q9F024	Q9f024 homo sapien
719	4	33.3	113	12	Q9IX48	Q9ix48 human enter	792	121	11	Q9CR41	Q9cr41 mus musculu
720	4	33.3	113	12	Q9IX47	Q9ix47 human enter	793	121	11	Q9CPV5	Q9cpv5 mus musculu
721	4	33.3	113	12	Q9IX46	Q9ix46 human enter	794	121	11	Q9CPV5	Q9cpv5 pseudomonas
722	4	33.3	113	12	Q9IX45	Q9ix45 human enter	795	121	16	Q916V3	Q916v3 pseudomonas
723	4	33.3	113	12	Q9IX44	Q9ix44 human enter	796	121	17	Q96ZF7	Q96zf7 sulfolobus
724	4	33.3	113	12	Q9IX43	Q9ix43 human enter	797	122	2	Q9F928	Q9f928 pseudomonas
725	4	33.3	113	12	Q9IX42	Q9ix42 human enter	798	122	2	Q9RNG8	Q9rng8 pseudomonas
726	4	33.3	113	12	Q9IX41	Q9ix41 human enter	799	122	2	P96778	P96778 haemophilus
727	4	33.3	113	12	Q9IX40	Q9ix40 human enter	800	122	3	Q93905	Q93905 neurospora
728	4	33.3	113	12	Q9IX39	Q9ix39 human enter	801	122	10	Q97361	Q97361 phytophthor
729	4	33.3	113	12	Q9IX38	Q9ix38 human enter	802	122	12	Q9ICF5	Q9icf5 fowlpox vir
730	4	33.3	113	12	Q9IX37	Q9ix37 human enter	803	122	12	Q9WYT9	Q9wyt9 thermotoda
731	4	33.3	113	12	Q9IX36	Q9ix36 human enter	804	122	16	Q9WYT9	Q9rha3 bruceella ab
732	4	33.3	113	12	Q9IX35	Q9ix35 human enter	805	123	2	Q9RHA3	Q9rs3w1 vibrio chol
733	4	33.3	113	12	Q9IX34	Q9ix34 human enter	806	123	2	Q9RHA3	Q9rs3w1 vibrio chol
734	4	33.3	114	2	P96779	P96779 haemophilus	807	123	2	Q9S3W1	Q9sgd1 zea mays (m
735	4	33.3	114	17	O59113	O59113 pyrococcus	808	123	2	Q9SGD1	Q9sgd1 zea mays (m
736	4	33.3	114	17	Q9YF31	Q9yf31 aeropyrum p	809	123	10	Q9XGD1	Q9xgd1 zea mays (m
737	4	33.3	114	17	Q96YK4	Q96yk4 sulfolobus	810	123	16	P74138	P74138 synecocyst
738	4	33.3	115	3	O13546	O13546 saccharomyc	811	123	16	P74138	P74138 synecocyst
739	4	33.3	115	3	Q9P7V2	Q9p7v2 schizosacch	812	123	16	Q51512	Q51512 pseudomonas
740	4	33.3	115	4	Q9C018	Q9c018 homo sapien	813	123	16	Q51512	Q51512 pseudomonas
741	4	33.3	115	4	Q9NAG8	Q9na98 caenorhabdi	814	123	16	Q98LV5	Q98lv5 rhizobium l
742	4	33.3	115	9	Q38444	Q38444 bacterioph	815	123	16	Q97NH5	Q97nh5 streptococ
743	4	33.3	115	13	Q9DDJ7	Q9ddj7 gallus gall	816	123	16	Q52888	Q52888 rhizobium m
744	4	33.3	115	17	Q9HNY1	Q9hny1 halobacteri	817	123	16	Q98C17	Q98ci17 rhizobium l
745	4	33.3	115	17	Q979N5	Q979n5 thermoplas	818	125	2	P78264	P78264 escherichia
746	4	33.3	116	2	P96776	P96776 haemophilus	819	125	2	Q9RCJ4	Q9rcj4 streptococ

966 4 33.3 144 16 Q97NG2 streptococc
967 4 33.3 144 16 Q92IL8 rickettsia
968 4 33.3 145 2 Q9LAG1 bacillus th
969 4 33.3 145 2 Q44017 alcaligenes
970 4 33.3 145 4 Q9NPX1
971 4 33.3 145 10 P93293
972 4 33.3 145 10 Q49553
973 4 33.3 145 16 Q9PM11
974 4 33.3 145 16 Q9S4X4
975 4 33.3 145 17 Q9Y800
976 4 33.3 146 2 Q53925
977 4 33.3 146 2 Q85750
978 4 33.3 146 3 Q04298
979 4 33.3 146 3 Q9LPA9
980 4 33.3 146 10 Q9V224
981 4 33.3 146 17 Q9V224
982 4 33.3 147 2 Q9RNE9
983 4 33.3 147 4 Q9BXL9
984 4 33.3 147 5 Q9GUS6
985 4 33.3 147 10 Q49862
986 4 33.3 147 10 Q49867
987 4 33.3 147 16 P74066
988 4 33.3 147 16 P73006
989 4 33.3 147 16 Q98JH5
990 4 33.3 147 17 Q58013
991 4 33.3 148 11 Q9CXA5
992 4 33.3 148 11 Q55104
993 4 33.3 148 12 Q9WIJ2
994 4 33.3 148 12 Q9WIJ3
995 4 33.3 148 16 Q92QJ9
996 4 33.3 148 17 Q9U2M2
997 4 33.3 149 2 Q9AJM2
998 4 33.3 149 2 Q68044
999 4 33.3 149 2 Q9S6G5
1000 4 33.3 149 2 Q9REV5

ALIGNMENTS

RESULT 1
Q9UC8 ID Q9UC8 PRELIMINARY; PRT; 19 AA.
AC Q9UC8
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE BETA-AMYLOID-(1-42) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94068497; PubMed=8248178;
RA Rohrer A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
RA Gowing E., Ball M.J.;
RT "beta-Amyloid-(1-42) is a major component of cerebrovascular amyloid
RT deposits: implications for the pathology of Alzheimer disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
DR HSSP; P05067; IAMB.
SQ SEQUENCE 19 AA; 2315 MW; 05B02B3F6DCE3E CRC64;

Query Match 100.0%; Score 12; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12

RESULT 2
Q9UCD1 ID Q9UCD1 PRELIMINARY; PRT; 28 AA.
AC Q9UCD1
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94045685; PubMed=8229004;
RA Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT "Characterization of beta-amyloid peptide from human cerebrospinal
RT fluid.";
RL J. Neurochem. 61:1965-1968(1993).
DR HSSP; P05067; IAMB.
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;
Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
RESULT 3
Q9UCA9 ID Q9UCA9 PRELIMINARY; PRT; 30 AA.
AC Q9UCA9
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BETA-AMYLOID PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
RT Alzheimer's disease patient.";
RL Ann. Neurol. 35:245-246(1994).
DR HSSP; P05067; IBA4.
SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match 100.0%; Score 12; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEV 12
Db 1 DAEFRHDSGYEV 12
RESULT 4
Q9UC33 ID Q9UC33 PRELIMINARY; PRT; 33 AA.
AC Q9UC33
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93024877; PubMed=1406936;
 RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
 RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.,
 RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
 RT biological fluids.";
 RL Nature 359:325-327(1992).
 DR HSSP: P05067; 1BA4.
 SQ SEQUENCE 33 AA; 3674 MW; B1DFE2F4167ABD0 CRC64;

Query Match 100.0%; Score 12; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
 Db 1 DAEFRHDSGYEV 12

RESULT 5
 ID P78438 PRELIMINARY; PRT; 82 AA.
 AC P78438;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
 GN APP.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor.";
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [2]

RP SEQUENCE OF 19-48 FROM N.A.
 RX MEDLINE=87120329; PubMed=2949367;
 RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
 RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
 RT "Amyloid beta protein gene: CDNA, mRNA distribution, and genetic
 RT linkage near the Alzheimer locus.";
 RL Science 235:880-884(1987).
 RN [3]

RP SEQUENCE OF 32-63 FROM N.A.
 RX MEDLINE=93035397; PubMed=1415269;
 RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
 RA Anderson L., O'dahl S., Nemens E., White J.A.;
 RT "Linkage and mutational analysis of familial Alzheimer disease
 RT kindreds for the APP gene region.";
 RL Am. J. Hum. Genet. 51:998-1014(1992).
 DR ENBL: M29270; AAA51768.1;
 DR ENBL: M29269; AAA51768.1;
 DR ENBL: M15532; AAA51564.1;
 DR ENBL: S45136; AAB23646.1;
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 12; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 8.5e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
 Db 17 DAEFRHDSGYEV 28

RESULT 6
 ID Q16014 PRELIMINARY; PRT; 82 AA.
 AC Q16014;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR ENBL: S60721; AAB26263.2;
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 12; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 8.5e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
 Db 18 DAEFRHDSGYEV 29

RESULT 7
 ID Q16019 PRELIMINARY; PRT; 82 AA.
 AC Q16019;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR ENBL: S61380; AAB26264.2;
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 12; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 8.5e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
|||||
Db 436 DAEFRHDSGYEV 447

RESULT 10

Q9PVL1 PRELIMINARY; PRT: 569 AA.
ID Q9PVL1
AC Q9PVL1
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=BRAIN;
RC Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RA "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 100.0%; Score 12; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
|||||
Db 472 DAEFRHDSGYEV 483

RESULT 11

Q95KN7 PRELIMINARY; PRT: 695 AA.
ID Q95KN7
AC Q95KN7
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=CEREBELLUM;
RC MEDLINE=91273117; PubMed=1905108;
RX Podlisy M.B., Tolan D.R., Selkoe D.J.;
RA "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease."
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.

Query Match 100.0%; Score 12; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 DAEFRHDSGYEV 29

RESULT 8

Q16020 PRELIMINARY; PRT: 82 AA.
ID Q16020
AC Q16020
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61363; AAB26265.2; -.
DR HSSP; P05067; 1BA4.
DR NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 12; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
|||||
Db 18 DAEFRHDSGYEV 29

RESULT 9

O93296 PRELIMINARY; PRT: 534 AA.
ID O93296
AC O93296
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98377885; PubMed=9671674;
RX Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons."
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 12; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 4e-06;

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FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 12; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
   |||||
Db 597 DAEFRHDSGYEV 608

RESULT 12
Q0496
ID Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
   alternative splicing.";
RL Blochlin. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 12; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
   |||||
Db 597 DAEFRHDSGYEV 608

RESULT 13
Q9DGJ8
ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX Sarasa M., Rodollosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
   isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 12; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
   |||||
Db 597 DAEFRHDSGYEV 608

RESULT 13
Q9DGJ8
ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX Sarasa M., Rodollosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
   isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -.

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DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 12; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
   |||||
Db 597 DAEFRHDSGYEV 608

RESULT 14
Q9DGJ7
ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX Sarasa M., Rodollosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
   isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289219; AAG00594.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 12; DB 13; Length 751;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
   |||||
Db 653 DAEFRHDSGYEV 664

RESULT 15
Q9TUI0
ID Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAA84580.1; -
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00114; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BC583E CRC64;

Query Match 100.0%; Score 12; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 672 DAEFRHDSGYEV 683

RESULT 16
Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldhaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR NON_TER 1
FT SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

Query Match 83.3%; Score 10; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EFRHDSGYEV 12
Db 1 EFRHDSGYEV 10

RESULT 17
Q9A4N9 PRELIMINARY; PRT; 528 AA.
ID Q9A4N9
AC Q9A4N9;

Query Match 58.3%; Score 7; DB 16; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HDSGYEV 12
Db 219 HDSGYEV 225

RESULT 18
Q53951 PRELIMINARY; PRT; 123 AA.
ID Q53951
AC Q53951;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ASPARTATE AMINOTRANSFERASE (FRAGMENT).
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomyces; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=95231511; PubMed=7715599;
RA Puttkhant C., Nihira T., Yamada Y.;
RT "Cloning, nucleotide sequence, and transcriptional analysis of the nusG gene of Streptomyces coelicolor A3(2), which encodes a putative transcriptional antiterminator.";
RL Mol. Gen. Genet. 247:118-122(1995).
DR EMBL; D32254; BAA21035.1; -.
DR HSSP; Q56232; 1BJW.
DR InterPro; IPR003662; sub_transporter.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Transferase; Aminotransferase.
FT NON_TER 123 123
FT SEQUENCE 123 AA; 12765 MW; B01B3B59BE7D1C2B CRC64;

Query Match 50.0%; Score 6; DB 2; Length 123;

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Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
Db 93 DSGYEV 98

RESULT 19
Q92PX4
ID Q92PX4 PRELIMINARY; PRT; 240 AA.
AC Q92PX4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE HYPOTHETICAL PROTEIN SMC01196.
GN SMC01196.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorhoelster F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti."
RL Science 293:668-672(2001).
DR EMBL: AL591787; CAC46176.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 240 AA; 27843 MW; 47C961CC62A24926 CRC64;

Query Match 50.0%; Score 6; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFPHD 7
Db 186 AEFPHD 191

RESULT 20
Q9AQL8
ID Q9AQL8 PRELIMINARY; PRT; 265 AA.
AC Q9AQL8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE HYPOTHETICAL 29.5 KDA PROTEIN.
OS Pseudomonas sp. CA10.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=135214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA10;
RX MEDLINE=21264379; PubMed=11371531;
RA Nojiri H., Sekiguchi H., Maeda K., Urata M., Nakai S., Yoshida T.,
RA Habe H., Omori T.;
RT "Genetic characterization and evolutionary implications of car gene
RL J. Bacteriol. 183:3663-3679(2001).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=CA10;
RX MEDLINE=97386424; PubMed=9244273;
RA Sato S., Ochiyama N., Kimura T., Nojiri H., Yamane H., Omori T.;
RT "Cloning of genes involved in carbazole degradation of Pseudomonas sp.
RT strain CA10: nucleotide sequence of genes and characterization of
RT meta-cleavage enzymes and hydrolase."
RL J. Bacteriol. 179:4841-4849(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CA10;
RX MEDLINE=97386425; PubMed=9244274;
RA Sato S., Nam J., Kasuga K., Nojiri H., Yamane H., Omori T.;
RT "Identification and characterization of genes encoding carbazole 1,9a-
RT dioxygenase in Pseudomonas sp. strain CA10."
RL J. Bacteriol. 179:4850-4858(1997).
DR EMBL: AB047548; BAB32778.1; -.
KW Hypothetical protein.
SQ SEQUENCE 265 AA; 29535 MW; 3406326573285C7D CRC64;

Query Match 50.0%; Score 6; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPFH 6
Db 242 DAEPFH 247

RESULT 21
Q9VID7
ID Q9VID7 PRELIMINARY; PRT; 279 AA.
AC Q9VID7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE CG8674 PROTEIN.
GN CG8674.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalaali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M., Pan S., Pollar J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AF003669; AAF53985.1; -.
DR FlyBase; FBgn0032937; CG8674.
SQ SEQUENCE 279 AA; 31860 MW; 16547409E226A853 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 279;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
Db 50 DSGYEV 55

RESULT 22
Q95YK6 PRELIMINARY; PRT; 372 AA.
AC Q95YK6; 2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEFTY/ANTIVIN RELATED PROTEIN.
GN CS-LFAN.
OS Ciona savignyi.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
OC Clonidae; Ciona.
OX NCBI_TaxID=51511;
RN [1]
RP SEQUENCE FROM N.A.
RA Satou Y., Imai K.S., Satoh N.;
RT "Ciona savignyi genes.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057739; BAB68348.1; -.
SQ SEQUENCE 372 AA; 42399 MW; A480E2EB5BE2D093 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 372;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
Db 367 DSGYEV 372

RESULT 23
Q30016 PRELIMINARY; PRT; 380 AA.
AC Q30016; 2001 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE BRANCHED-CHAIN AMINO ACID ABC TRANSPORTER, PERIPLASMIC BINDING PROTEIN
DE (BRAC-1).
GN AF0223.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Kyrpides N.C.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Sutton G.G., Gill S.,
RA Fleckmann R.D., Quackenbush J., Lee N.H., Adams M.D., Loftus B.,
RA Kirschner E.F., Dougherty B.A., McKenney K., Glodek A., Zhou L.,
RA Peterson S., Reich C.J., McNeil L.K., Badger J.H., Utterback T.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AF001090; AAB91009.1; -.
DR TIGR; AF0223; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 380 AA; 42604 MW; 94F24F75B0DC5FB CRC64;

Query Match 50.0%; Score 6; DB 17; Length 380;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
Db 131 DSGYEV 136

RESULT 24
Q9L0L5 PRELIMINARY; PRT; 408 AA.
AC Q9L0L5; 2001 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ASPARTATE AMINOTRANSFERASE.
GN ASPC.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-1 OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; AL160431; CAB77419.1; -.
DR HSSP; Q56232; 1BJW.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR InterPro; IPR003662; sub_transporter.
DR PRINTS; PR00753; ACCSYNTHASE.

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DR PROSITE: PS00105; AA_TRANSFER_CLASS.1; 1.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN.1.
 KW Aminotransferase; Pyridoxal phosphate; Transferase.
 SQ SEQUENCE 408 AA; 43482 MW; 4D0B84D479D5A007 CRC64;

Query Match 50.0%; Score 6; DB 2; Length 408;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 DSGYEV 12
 |||||
 Db 93 DSGYEV 98

RESULT 25
 Q9KY96 PRELIMINARY; PRT; 418 AA.
 ID Q9KY96
 AC Q9KY96;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE PUTATIVE SEPTUM SITE-DETERMINING PROTEIN.
 GN MIND1.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MEDLINE=37000351; PubMed=8843436;
 RX Redenbach M., Kieser H.M., Denapalae D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; AL356813; CAB92599.1; -.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF00991; Para; 1.
 DR SMART; SM00448; REC; 1.
 SQ SEQUENCE 418 AA; 43352 MW; C1BFE49507E63BD6 CRC64;

Query Match 50.0%; Score 6; DB 2; Length 418;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FRHDSG 9
 |||||
 Db 224 FRHDSG 229

RESULT 26
 Q93RK7 PRELIMINARY; PRT; 432 AA.
 ID Q93RK7
 AC Q93RK7;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE REPLICATION PROTEIN.
 GN REP 43.

OS Bacillus sp. KSM-KP43.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=109322;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KSM-KP43;
 RA Hatada Y., Ito S.;
 RT "A novel plasmid isolated from an alkaline Bacillus strain."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB034994; BAB58973.1; -.
 SQ SEQUENCE 432 AA; 50516 MW; 27ADF6DC21C1182 CRC64;

Query Match 50.0%; Score 6; DB 2; Length 432;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AEFRHD 7
 |||||
 Db 183 AEFRHD 188

RESULT 27
 Q941F1 PRELIMINARY; PRT; 444 AA.
 ID Q941F1
 AC Q941F1;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE AT1G06800/F4H5.10.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesena E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY052199; AAK97670.1; -.
 SQ SEQUENCE 444 AA; 50184 MW; C3BD4E0AA9723351 CRC64;

Query Match 50.0%; Score 6; DB 10; Length 444;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 DSGYEV 12
 |||||
 Db 154 DSGYEV 159

RESULT 28
 O04340 PRELIMINARY; PRT; 447 AA.
 ID O04340
 AC O04340;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PUTATIVE LIPASE.
 GN AT2G30550.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U93215; AAB63082.1; -.
 DR InterPro: IPR000379; Est_lip_thioest_actsite.
 DR InterPro: IPR000734; Lipase_3.
 DR Pfam: PF01764; Lipase_3; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 SQ SEQUENCE 447 AA; 51309 MW; 6C0B8BF1C64E757C CRC64;

Query Match 50.0%; Score 6; DB 10; Length 447;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
 |||||
 Db 88 DSGYEV 93

RESULT 29
 ID O30322 PRELIMINARY; PRT; 453 AA.
 AC O30322; 1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE HYPOTHETICAL 52.4 KDA PROTEIN.
 GN AF2347.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 OC Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98045343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kervilave A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 RA Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus";
 RL Nature 390:364-370(1997).
 DR EMBL; AE001114; AAB91316.1; -.
 DR TIGR; AF2347; -.
 DR InterPro: IPR002052; N6_Mtase.

DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 453 AA; 52365 MW; 8B0AD84A99C80577 CRC64;

Query Match 50.0%; Score 6; DB 17; Length 453;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
 |||||
 Db 107 DSGYEV 112

RESULT 30
 ID Q9M9Y7 PRELIMINARY; PRT; 515 AA.
 AC Q9M9Y7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE F4H5.11 PROTEIN.
 GN F4H5.11.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altati H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
 RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC011001; AAF63138.1; -.
 DR InterPro: IPR000379; Est_lip_thioest_actsite.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR002921; Lipase_3.
 DR Pfam: PF01764; Lipase_3; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 SQ SEQUENCE 515 AA; 58445 MW; DD59442CB9166451 CRC64;

Query Match 50.0%; Score 6; DB 10; Length 515;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
 |||||
 Db 154 DSGYEV 159

RESULT 31
 ID O08569 PRELIMINARY; PRT; 533 AA.
 AC O08569;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ACROSOMAL MATRIX COMPONENT AM67 PRECURSOR.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HARTLEY; TISSUE=TESTIS;
 RX MEDLINE=97284752; PubMed=9139729;
 RA Foster J.A., Friday B.B., Maulit M.T., Blobel C., Winfrey V.P.,
 RA Olson G.E., Kim K.S., Gerton G.L.;
 RT "AM67, a secretory component of the guinea pig sperm acrosomal matrix,

RT is related to mouse sperm protein sp56 and the complement component 4-
 RL binding proteins.";
 J. Biol. Chem. 272:12714-12722(1997).
 DR EMBL; U75654; AAC13888.1; -;
 DR HSSP; P10998; 1VVD;
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00084; sushi; 7.
 DR SMART; SM00032; CCP; 7.
 KW SIGNAL.
 FT SIGNAL.
 FT CHAIN 1 28 POTENTIAL.
 FT CHAIN 29 533 ACROSOMAL MATRIX COMPONENT AM67.
 SQ SEQUENCE 533 AA; 59772 MW; EDBDDE487A45389 CRC64;

Query Match 50.0%; Score 6; DB 11; Length 533;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSGYEV 12
 Db 439 DSGYEV 444
 |||||

RESULT 32
 Q952X3 PRELIMINARY; PRT; 576 AA.
 AC Q952X3;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN C34F11.9A.
 GN C34F11.9
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;

RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;

RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Bentley D.;
 RT "The sequence of C. elegans cosmid C34F11.9";
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U46753; AAK68220.1; -;
 SQ SEQUENCE 576 AA; 64138 MW; 7781DBE10E3AB1F6 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 576;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSGYEV 12
 Db 120 DSGYEV 125
 |||||

RESULT 33
 Q952X4 PRELIMINARY; PRT; 642 AA.
 ID Q952X4
 AC Q952X4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN C34F11.9C.
 GN C34F11.9
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;

RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX Bentley D.;
 RT "The sequence of C. elegans cosmid C34F11.9";
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U46753; AAK68221.1; -;
 SQ SEQUENCE 642 AA; 71159 MW; A2965E8D34F8063A CRC64;

Query Match 50.0%; Score 6; DB 5; Length 642;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSGYEV 12
 Db 120 DSGYEV 125
 |||||

RESULT 34
 O57394 PRELIMINARY; PRT; 699 AA.
 ID O57394;
 AC O57394;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE EL AMYLOID PRECURSOR PROTEIN 699.
 GN EL APP699.
 OS Narke japonica (Electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogoralea; Batoidae;
 OC Torpediniformes; Narcinoidei; Narkidae; Narke.
 OX NCBI_TaxID=62965;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ELECTRIC LOBE;
 RX MEDLINE=98129705; PubMed=9461486;
 RA Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
 RA Suzuki T.;
 RT "cDNA isolation of Alzheimer's amyloid precursor protein from
 RT cholinergic nerve terminals of the electric organ of the electric
 RT ray.";
 RL Biochem. J. 330:29-33(1998).
 DR EMBL; AB005544; BAA24230.1; -;
 DR HSSP; P05067; 1H23.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE: PS00320; A4_INTRA: 1.
SQ SEQUENCE 699 AA; 78879 MW; 952915C309D50E5C CRC64;

Query Match 50.0%; Score 6; DB 13; Length 699;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
DB 607 DSGYEV 612

RESULT 35

Q9TX98 PRELIMINARY; PRT; 39 AA.

AC Q9TY98;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GLP-1 PROTEIN (FRAGMENT).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93091267; PubMed=1457827;
RA Kodoyianni V., Maine E.M., Kimble J.;
RT "Molecular basis of loss-of-function mutations in the glp-1 gene of
RT Caenorhabditis elegans";
RL Mol. Biol. Cell 3:1199-1213(1992).
DR InterPro: IPR000561; EGF-like.
DR SMART: SM00181; EGF; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 39 AA; 4530 MW; 276064C265E19927 CRC64;

Query Match 41.7%; Score 5; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYE 11
DB 30 DSGYE 34

RESULT 36

O87879 PRELIMINARY; PRT; 105 AA.

AC O87879;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE REGULATORY PROTEIN (FRAGMENT).
GN ORP4.
OS Thauera aromatica.
OC Bacteria; Proteobacteria; beta subdivision; Rhodocyclus group;
OC Thauera;
OX NCBI_TaxID=59405;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98417440; PubMed=9746358;
RA Breese K., Boll M., Alt-Moerbe J., Schaeffer H., Fuchs G.;
RT "Genes coding for the benzoyl-CoA pathway of anaerobic aromatic
RT metabolism in the bacterium Thauera aromatica.";
RL Eur. J. Biochem. 256:148-154(1998).
DR EMBL: AJ224959; CAA1253.1; -.
FT NON_TER 105
SQ SEQUENCE 105 AA; 11717 MW; 537D72B24364DA3 CRC64;

Query Match 41.7%; Score 5; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHDG 9
DB 56 RHDG 60

RESULT 37

Q9W5B9 PRELIMINARY; PRT; 107 AA.

AC Q9W5B9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE CG11639 PROTEIN.
GN TFIIA-S-2 OR EG:BACF7A4.7 OR CG11639.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de la Cruz A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003419; AAF45575.1; -.
DR HSSP: P32774; YTF.
DR FlyBase: FBgn0040338; TFIIA-S-2.
DR InterPro: IPR003194; TFIIA_gamma.
DR Pfam: PF02268; TFIIA_gamma; 1.
DR Pfam: PF02751; TFIIA_gamma-C; 1.
SQ SEQUENCE 107 AA; 12273 MW; C6545CDDF3A65E44 CRC64;

Query Match 41.7%; Score 5; DB 5; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
 Db 79 DAEFR 83

RESULT 38
 Q9DH37 PRELIMINARY; PRT; 108 AA.
 AC Q9DH37;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE HYPOTHETICAL 12.0 KDA PROTEIN.
 GN MDV082 OR MDV102.
 OS Turkey herpesvirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
 OX NCBI_TaxID=10390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MD5;
 RX MEDLINE=20392152; PubMed=10933706;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
 RT "The genome of a very virulent Marek's disease virus";
 RL J. Virol. 74:7980-7988(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MD5;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF243438; AAG14285.1; -;
 DR EMBL; AF243438; AAG14274.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 108 AA; 12031 MW; 67DD21868D9B0AD7 CRC64;

Query Match 41.7%; Score 5; DB 12; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RHDSG 9
 Db 20 RHDSG 24

RESULT 39
 Q9F8D1 PRELIMINARY; PRT; 111 AA.
 AC Q9F8D1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE HYPOTHETICAL 12.3 KDA PROTEIN (FRAGMENT).
 OS Rhizobium etli.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=29449;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CE3H7;
 RX MEDLINE=20466936; PubMed=11010872;
 RA Bascones E., Imperial J., Ruiz-Argueso T., Palacios J.M.;
 RT "Generation of new hydrogen-recycling rhizobiaceae strains by
 introduction of a novel hup mini-transposon";
 RL Appl. Environ. Microbiol. 66:4292-4299(2000).
 DR EMBL; AF247185; AAG28602.1; -;
 KW Hypothetical protein.
 FT NON-TER 111 111
 SQ SEQUENCE 111 AA; 12334 MW; D2970360028D8640 CRC64;

Query Match 41.7%; Score 5; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
 Db 43 DAEFR 47

RESULT 40
 Q9Z6Z9 PRELIMINARY; PRT; 112 AA.
 AC Q9Z6Z9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PERIPLASMIC DIVALENT CATION TOLERANCE PROTEIN.
 GN CUTA OR CPN0907 OR CP0959.
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99266606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 pneumoniae AR39";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JL38;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 DR EMBL; A5001671; AAD19045.1; -;
 DR EMBL; A5002253; AAF38739.1; -;
 DR EMBL; AF002548; BAA99115.1; -;
 DR TIGR; CP0959; -;
 DR InterPro; IPR004323; CutA1.
 DR Pfam; PF03091; CutA1; 1.
 KW Complete proteome.
 SQ SEQUENCE 112 AA; 12793 MW; CFB46DF27EF7EA2C CRC64;

Query Match 41.7%; Score 5; DB 16; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
 Db 76 SGYEV 80

RESULT 41
 Q94KV8 PRELIMINARY; PRT; 115 AA.
 ID Q94KV8

AC Q94KV8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE THIOGLUCOSIDE GLUCOHYDROLASE 2 (FRAGMENT).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. YUDAL;
RA Fourmann M., Froger N., Brunel D.;
RT "Amplified consensus gene markers: Tools for designing a genetic map
of Arabidopsis-known-function genes in Brassica."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF261100; AAK49404.1; -.
KW Hydrolase.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 12760 MW; 801F948683FD96EB CRC64;

Query Match 41.7%; Score 5; DB 10; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
Db 13 SGYEV 17

RESULT 42
Q97Y29 PRELIMINARY; PRT; 117 AA.
AC Q97Y29;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE HYPOTHETICAL PROTEIN SSO1520.
GN SSO1520.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Eraso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sengen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
RL EMBL; AE006767; AAK41742.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 117 AA; 13930 MW; 3420E14682494C64 CRC64;

Query Match 41.7%; Score 5; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYE 11
Db 73 DSGYE 77

RESULT 43

Q9J0D7 PRELIMINARY; PRT; 120 AA.
AC Q9J0D7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Human coxsackievirus B2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus
OX NCBI_TaxID=82639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
EX MEDLINE=20472678; PubMed=11015360;
RA Peng T., Li Y., Yang Y., Niu C., Morgan-Capner P., Archard L.C.,
RA Zhang H.;
RT "Characterization of Enterovirus Isolates from Patients with Heart
Muscle Disease in a Selenium-Deficient Area of China."
RL J. Clin. Microbiol. 38:3538-3543(2000).
DR EMBL; AF225467; AAF44100.1; -.
DR HSP; Q83744; IGOV.
DR InterPro; IPR001676; Rnv.
DR Pfam; PF00073; rnv; 1.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13732 MW; F02AF18A4B4EBFD1 CRC64;

Query Match 41.7%; Score 5; DB 12; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EPRHD 7
Db 40 EPRHD 44

RESULT 44
Q9QZV0 PRELIMINARY; PRT; 124 AA.
AC Q9QZV0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE AD1-ANTIGEN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=OVARY;
RA Espey L.L., Ujioaka T., Okamura H., Richards J.S.;
RT "Characterization of ovarian ad1-antigen gene expression during
ovulation in the gonadotropin-primed immature rat."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159104; AAD56635.1; -.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4; 1.
FT NON_TER 1
SQ SEQUENCE 124 AA; 13839 MW; D1A0DB25FC9EB19D CRC64;

Query Match 41.7%; Score 5; DB 11; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SGYEV 12
Db 119 SGYEV 123

RESULT 43

RESULT 45
Q9EYQ6 PRELIMINARY; PRT; 128 AA.
AC Q9EYQ6:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE RIBOSOMAL PROTEIN S12 (FRAGMENT).
GN RPSL.
OS Thermus thermophilus.
OC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IB-21;
RA Gregory S.T., Dahlberg A.E., Cate J.H.;
RT "Streptomycin-resistant and streptomycin-dependent mutants of the
RT extreme thermophile Thermus thermophilus IB-21."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF316617; AAG38586.1; -;
DR InterPro; IPR000230; Ribosomal_S12.
DR Pfam; PF00164; Ribosomal_S12; 1.
DR PRINTS; PR01034; RIBOSOMALS12.
DR ProDom; PD000576; Ribosomal_S12; 1.
DR PROSITE; PS00055; RIBOSOMAL_S12; 1.
FT NON_TER 1
SQ SEQUENCE 128 AA; 14157 MW; 52207FFD84B249FD CRC64;

Query Match 41.7%; Score 5; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SGYEV 12
Db 55 SGYEV 59

RESULT 46
Q9WRY3 PRELIMINARY; PRT; 130 AA.
AC Q9WRY3:
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VP1 (FRAGMENT).
OS Human coxsackievirus B2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=82639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FL92-1512;
RX MEDLINE=99221739; PubMed=10203472;
RA Oberste M.S., Maher K., Kilpatrick D.R., Flemister M.R., Brown B.A.,
RA Pallansch M.A.;
RT "Typing of human enteroviruses by partial sequencing of VP1."
RL J. Clin. Microbiol. 37:1288-1293(1999).
DR EMBL; AF081604; RAD40508.1; -;
DR HSSP; Q83744; ICOV.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; rhv; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 14847 MW; EB99725B40898B5C CRC64;

Query Match 41.7%; Score 5; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EFRHD 7
Db 49 EFRHD 53

Db 50 EFRHD 54
RESULT 47
Q9WRX4 PRELIMINARY; PRT; 130 AA.
AC Q9WRX4:
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VP1 (FRAGMENT).
OS Human coxsackievirus B2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=82639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC95-2135.
RX MEDLINE=99221739; PubMed=10203472;
RA Oberste M.S., Maher K., Kilpatrick D.R., Flemister M.R., Brown B.A.,
RA Pallansch M.A.;
RT "Typing of human enteroviruses by partial sequencing of VP1."
RL J. Clin. Microbiol. 37:1288-1293(1999).
DR EMBL; AF081621; AAD40525.1; -;
DR HSSP; Q83744; ICOV.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; rhv; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 14849 MW; EB99713B40898B5C CRC64;

Query Match 41.7%; Score 5; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EFRHD 7
Db 50 EFRHD 54

RESULT 48
Q91210 PRELIMINARY; PRT; 131 AA.
AC Q91210:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Human coxsackievirus B2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=82639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR/ROMA98;
RA Manzara S., Muscillo M., La Rosa G., Marianelli C., Cattani P.,
RA Fadda G.;
RT "Biological and molecular characterization of human enteroviruses."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ309266; CAC84703.1; -;
FT NON_TER 1
SQ SEQUENCE 131 AA; 14878 MW; 54B5BBAB6228508B CRC64;

Query Match 41.7%; Score 5; DB 12; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EFRHD 7
Db 49 EFRHD 53

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RESULT 49
Q9P6S6 PRELIMINARY; PRT; 132 AA.
ID Q9P6S6
AC Q9P6S6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PUTATIVE RNA POLYMERASE BETA-SUBUNIT.
GN SPC27.01C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaceae;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Seeger K., Wood V., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL353866; CAB89001.1; -.
SQ SEQUENCE 132 AA; 15636 MW; 91DD4C72ACEA6BD3 CRC64;

Query Match 41.7%; Score 5; DB 3; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 87 DAEFR 91

RESULT 50
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AC P78948;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE FISSION YEAST DNA FOR CHROMOSOME II COSMID 1228 SEQUENCE.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaceae;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Kohnosu A., Niwa O., Yano M., Saitoh S., Katayama T., Nagao K.,
RA Yanagida M.;
RT "S.pombe chromosome II cosmid 1228 sequence.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D83993; BAA12198.1; -.
SQ SEQUENCE 132 AA; 15658 MW; 31985823E354ABBE CRC64;

Query Match 41.7%; Score 5; DB 3; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFR 5
Db 87 DAEFR 91

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Search completed: September 13, 2002, 09:10:05
Job time: 235 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:03:29 ; Search time 30.09 Seconds
(without alignments)
44.297 Million cell updates/sec

Title: US-09-580-015-42_COPY_1_12
Perfect score: 12
Sequence: 1 DAEFRHDSGYEV 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	12	100.0	13	22	AA846198
2	12	100.0	13	22	AA846198
3	12	100.0	15	20	AA849094
4	12	100.0	15	20	AA849094
5	12	100.0	16	18	AA860371
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7	12	100.0	16	20	AA849693
8	12	100.0	17	21	AA849693
9	12	100.0	17	22	AA848345
10	12	100.0	21	20	AA808361
11	12	100.0	21	20	AA833755

12	100.0	21	22	AA847265	Peptide 5-16' SW, f
13	100.0	22	11	AA807753	Bta-amyloid prottri
14	100.0	28	10	AA80381	Synthetic A4 amylo
15	100.0	28	15	AA854702	Beta-amyloid fragm
16	100.0	28	15	AA860368	Beta-amyloid (1-28
17	100.0	28	16	AA864170	A4-O(1-28) a parti
18	100.0	28	16	AA864172	A4-O(1-28) a parti
19	100.0	28	17	AA801413	Beta/A4-amyloid pe
20	100.0	28	17	AA801414	Beta/A4-amyloid pe
21	100.0	28	20	AA839805	Beta-amyloid prote
22	100.0	28	20	AA839806	Beta-amyloid prote
23	100.0	28	20	AA84467	Synthetic amyloid
24	100.0	28	22	AA891783	Amyloid beta-prote
25	100.0	28	22	AA891789	Amyloid beta-prote
26	100.0	28	22	AA849396	Human amyloid pept
27	100.0	28	22	AA849396	Human amyloid pept
28	100.0	28	22	AA835590	Human clone B(1-28
29	100.0	28	22	AA835597	Human clone H130 B
30	100.0	28	22	AA835597	Human clone H130 B
31	100.0	28	22	AA835599	Human clone K16Q B
32	100.0	28	22	AA835599	Human clone K16Q B
33	100.0	28	22	AA836201	Human clone D230 B
34	100.0	28	22	AA836202	Human clone D230 B
35	100.0	30	20	AA841468	Synthetic amyloid
36	100.0	30	20	AA841468	Beta-secretase sub
37	100.0	33	20	AA833753	Amyloid precursor
38	100.0	33	20	AA898002	Synthetic amyloid
39	100.0	33	20	AA841469	Peptide 17-16' SW,
40	100.0	33	22	AA847263	Beta-amyloid pepti
41	100.0	35	17	AA802335	Beta-amyloid pepti
42	100.0	35	19	AA847228	Beta-amyloid pepti
43	100.0	35	20	AA893555	Beta-amyloid pepti
44	100.0	35	20	AA893559	Beta-amyloid pepti
45	100.0	35	20	AA893560	Beta-amyloid pepti
46	100.0	36	20	AA841471	Synthetic amyloid
47	100.0	38	15	AA860362	Beta-amyloid (1-38
48	100.0	38	20	AA892722	Human tachykinin a
49	100.0	38	22	AA891799	Amyloid beta-prote
50	100.0	38	22	AA891826	Amyloid beta-prote
51	100.0	39	15	AA860363	Beta-amyloid (1-39
52	100.0	39	20	AA825134	Human amyloid beta
53	100.0	39	20	AA841472	Synthetic amyloid
54	100.0	39	21	AA869717	Beta-APP alpha-sec
55	100.0	39	21	AA869718	Beta-APP alpha-sec
56	100.0	40	14	AA833191	Beta-amyloid pepti
57	100.0	40	15	AA860364	Beta-amyloid (1-40
58	100.0	40	18	AA837507	Amyloid beta prote
59	100.0	40	18	AA823335	Amyloid beta pepti
60	100.0	40	19	AA847232	Beta-amyloid pepti
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62	100.0	40	20	AA839339	Beta-amyloid prote
63	100.0	40	20	AA839804	Beta-amyloid prote
64	100.0	40	20	AA825135	Human amyloid beta
65	100.0	40	20	AA8414099	Human beta-amyloid
66	100.0	40	20	AA899584	Wild type aggregat
67	100.0	40	20	AA899584	Human tachykinin a
68	100.0	40	22	AA861473	Synthetic amyloid
69	100.0	40	22	AA805483	Human peptide anti
70	100.0	40	22	AA844426	Partial sequence o
71	100.0	40	22	AA891780	Amyloid beta-prote
72	100.0	40	22	AA891802	Amyloid beta-prote
73	100.0	40	22	AA891813	Amyloid beta-prote
74	100.0	40	22	AA891829	Amyloid beta-prote
75	100.0	41	13	AA82206	Alzheimer's amyloi
76	100.0	41	14	AA845230	Beta-amyloid prote
77	100.0	41	15	AA860365	Beta-amyloid (1-41
78	100.0	41	16	AA865283	Beta amyloid pepti
79	100.0	41	20	AA825136	Human amyloid beta
80	100.0	41	21	AA811497	Human amyloid beta
81	100.0	42	13	AA820330	Sequence of A99 (b
82	100.0	42	14	AA833192	Beta-amyloid pepti
83	100.0	42	15	AA860366	Beta-amyloid (1-42
84	100.0	42	16	AA865285	Beta amyloid pepti

85	12	100.0	42	16	AAR65286	Beta amyloid pepti	158	12	100.0	57	21	AAB10910	Human amyloid prec
86	12	100.0	42	16	AAR65287	Beta amyloid pepti	159	12	100.0	58	15	AAR58937	Amyloid precursor
87	12	100.0	42	16	AAR65288	Beta amyloid pepti	160	12	100.0	58	20	AAR98001	Swedish-FAD APP714
88	12	100.0	42	17	AAR95248	Beta/A4-amyloid pe	161	12	100.0	59	17	AAW05375	Amyloid precursor
89	12	100.0	42	17	AAR94591	Alzheimer amyloid	162	12	100.0	59	19	AAW70863	Beta-amyloid precu
90	12	100.0	42	18	AAW12828	Beta A4 peptide.	163	12	100.0	59	22	AAB84425	Partial sequence o
91	12	100.0	42	18	AAW08350	Wild type APP beta	164	12	100.0	60	19	AAW49007	Beta-amyloid precu
92	12	100.0	42	19	AAW64507	Neurotoxic beta-am	165	12	100.0	60	21	AAV69701	Homo sapiens beta-
93	12	100.0	42	19	AAW47230	Beta-amyloid pepti	166	12	100.0	63	18	AAW26511	Amyloid precursor
94	12	100.0	42	19	AAW42989	Full length beta-a	167	12	100.0	63	18	AAW26391	APP-REP 751 BAP pe
95	12	100.0	42	20	AAV33407	Human beta amyloid	168	12	100.0	63	19	AAW44747	APP-REP 751 [BAP E
96	12	100.0	42	20	AAV33752	Human amyloidogeni	169	12	100.0	63	19	AAW44746	Beta-amyloid pepti
97	12	100.0	42	20	AAV25137	Synthetic oligopep	170	12	100.0	63	19	AAW42975	Beta-amyloid pepti
98	12	100.0	42	20	AAV08607	Human beta-amyloid	171	12	100.0	63	19	AAW42976	Peptide derived fr
99	12	100.0	42	20	AAW29093	A-beta-binding pep	172	12	100.0	67	19	AAW71377	Human wild-type AP
100	12	100.0	42	20	AAW95985	Mutant aggregating	173	12	100.0	70	22	AAE09373	Human APP695 Swedi
101	12	100.0	42	20	AAW92726	Human tachykinin a	174	12	100.0	70	22	AAE09374	Human truncated AP
102	12	100.0	42	20	AAW81474	Synthetic amyloid	175	12	100.0	70	22	AAU05015	Human amyloid prec
103	12	100.0	42	21	AAV96956	Beta-amyloid 1-42	176	12	100.0	70	22	AAU05015	Novel human diagno
104	12	100.0	42	22	AAB82622	Amyloid-beta pepti	177	12	100.0	79	19	AAW53981	Sequence of A99 (b
105	12	100.0	42	22	AAE05484	Human peptide anti	178	12	100.0	93	22	ABG19083	Variant beta amylo
106	12	100.0	42	22	AAAB7262	Peptide 26-16' SW,	179	12	100.0	93	16	AAE64167	Beta-amyloid precu
107	12	100.0	42	22	AAAB6134	Human Alzheimer-be	180	12	100.0	99	16	AAE74694	Beta-amyloid precu
108	12	100.0	42	22	AAAB91779	Amyloid beta-prote	181	12	100.0	99	16	AAE74695	Beta-amyloid precu
109	12	100.0	42	22	AAAB91812	Amyloid beta-prote	182	12	100.0	99	16	AAE74696	Beta-amyloid precu
110	12	100.0	42	22	AAAB49098	Human amyloid beta	183	12	100.0	99	20	AAV08606	Human beta-amyloid
111	12	100.0	42	22	AAAB48497	Human amyloid prot	184	12	100.0	99	20	AAV08606	Human beta-amyloid
112	12	100.0	42	22	AAAB48830	Human amyloid-beta	185	12	100.0	99	22	AAB11483	Human APP peptide
113	12	100.0	42	22	AAAB49395	Human amyloid-beta	186	12	100.0	100	14	AAAB10024	Beta-amyloid-relat
114	12	100.0	42	22	AAAB35589	Beta/A4-amyloid pe	187	12	100.0	100	14	AAAB37866	Full-length beta-a
115	12	100.0	42	22	AAAP96371	Region of pre-APC	188	12	100.0	100	21	AAAB13015	Human amyloid prec
116	12	100.0	43	10	AAAP96371	Beta amyloid pepti	189	12	100.0	100	21	AAAB13015	Transgenic APP pro
117	12	100.0	43	15	AAAR34759	Beta-amyloid (1-43	190	12	100.0	103	16	AAAR74697	Beta-amyloid precu
118	12	100.0	43	15	AAAR60367	Amyloid beta-prote	191	12	100.0	103	16	AAAR74698	Beta-amyloid precu
119	12	100.0	43	15	AAAR61328	Beta amyloid prote	192	12	100.0	103	19	AAW51317	Natural beta-amylo
120	12	100.0	43	16	AAAR64165	A-beta protein (43	193	12	100.0	103	20	AAW89372	Beta-amyloid precu
121	12	100.0	43	17	AAAR95673	Human beta-amyloid	194	12	100.0	103	21	AAV56103	Beta-amyloid precu
122	12	100.0	43	18	AAW93371	Beta-amyloid pepti	195	12	100.0	104	19	AAE12509	Amino acid sequenc
123	12	100.0	43	19	AAV17758	Human amyloid precu	196	12	100.0	104	19	AAE12509	Familial Alzheimer
124	12	100.0	43	19	AAV71378	Natural beta-amylo	197	12	100.0	111	20	AAW93556	Swedish-FAD APP po
125	12	100.0	43	19	AAW51316	Human amyloid-beta	198	12	100.0	115	20	AAW97997	Swedish-FAD APP po
126	12	100.0	43	19	AAW40129	Beta-amyloid-beta	199	12	100.0	115	20	AAW97999	Swedish-FAD APP po
127	12	100.0	43	20	AAV42955	Beta-amyloid-beta	200	12	100.0	115	20	AAW98000	Swedish-FAD APP po
128	12	100.0	43	20	AAW92724	Human tachykinin a	201	12	100.0	116	21	AAV87823	Human APP signal p
129	12	100.0	43	20	AAW89373	Beta-amyloid pepti	202	12	100.0	116	21	AAV87823	Flag-amyloid prote
130	12	100.0	43	20	AAW89362	Beta-amyloid pepti	203	12	100.0	117	19	AAV51102	Transgenic APP pro
131	12	100.0	43	21	AAAB27020	Beta-amyloid pepti	204	12	100.0	117	22	AAE12896	Human recombinant
132	12	100.0	43	21	AAAB15372	Human beta-amyloid	205	12	100.0	118	19	AAW50029	APP C-terminal fra
133	12	100.0	43	21	AAAB21216	Beta-amyloid pepti	206	12	100.0	118	19	AAW50030	APP C-terminal fra
134	12	100.0	43	21	AAV88390	Human beta-amyloid	207	12	100.0	118	19	AAW50027	APP C-terminal fra
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136	12	100.0	43	22	AAV78791	Natural beta amylo	209	12	100.0	118	19	AAW50028	APP C-terminal fra
137	12	100.0	43	22	AAAG78791	Beta-amyloid pepti	210	12	100.0	118	20	AAW96209	APP C-terminal fra
138	12	100.0	43	22	AAAB84428	Human beta amyloid	211	12	100.0	120	19	AAW50032	Amyloid precursor
139	12	100.0	43	22	AAAB84428	Partial sequence o	212	12	100.0	120	19	AAW50032	APP C-terminal fra
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141	12	100.0	43	22	AAAB81193	Amyloid beta-prote	214	12	100.0	124	21	AAV96955	Human beta amyloid
142	12	100.0	43	22	AAAB91778	Amyloid beta-prote	215	12	100.0	132	16	AAE65291	Deduced sequence i
143	12	100.0	43	22	AAAB91811	Beta-amyloid pepti	216	12	100.0	162	9	AAE65291	Beta-amyloid-relat
144	12	100.0	43	22	AAAB47108	Variant beta amylo	217	12	100.0	162	12	AAAR10023	Deduced from clone
145	12	100.0	45	16	AAAB48344	Synthetic amyloid	218	12	100.0	162	14	AAAR37863	Beta-amyloid precu
146	12	100.0	47	20	AAW81475	Variant beta amylo	219	12	100.0	249	15	AAE65798	Protein sequence 1
147	12	100.0	48	22	AAAB37523	Synthetic amyloid	220	12	100.0	264	10	AAAP90497	Sequence of amy 37
148	12	100.0	50	22	AAAG5957	Amyloid precursor	221	12	100.0	264	10	AAAP90609	Amyloid precursor
149	12	100.0	51	19	AAW53984	Human A4 amyloid p	222	12	100.0	487	18	AAW26510	Amyloid precursor
150	12	100.0	52	16	AAAR64166	Human A4 amyloid p	223	12	100.0	487	18	AAW26510	APP-REP 751 protei
151	12	100.0	52	20	AAW81476	Variant beta amylo	224	12	100.0	487	19	AAW44745	Amyloid precursor
152	12	100.0	53	15	AAAR55695	Synthetic amyloid	225	12	100.0	492	14	AAAR42979	APP-REP 751 amyloi
153	12	100.0	53	15	AAAR55696	Sequence of uniden	226	12	100.0	492	18	AAAR45229	Amyloid precursor
154	12	100.0	53	15	AAAR55697	Sequence of uniden	227	12	100.0	492	18	AAW26393	Amyloid precursor
155	12	100.0	53	16	AAAR64168	Variant beta amylo	228	12	100.0	492	19	AAW44744	APP-REP 751 protei
156	12	100.0	54	21	AAAB32126	Amyloid-beta precu	229	12	100.0	492	19	AAW44744	Amyloid precursor
157	12	100.0	55	22	AAB11482	Human APP peptide	230	12	100.0	506	19	AAW611152	Maltose binding pr

231	12	100.0	304	12	100.0	751	18	AAW19499	APP751 mutant A-be
232	12	100.0	305	12	100.0	751	18	AAW19483	APP751 mutant A-be
233	12	100.0	306	12	100.0	751	18	AAW19492	APP751 mutant A-be
234	12	100.0	307	12	100.0	751	20	AAW08615	Human beta-amyloid
235	12	100.0	308	12	100.0	751	20	AAW08605	Human beta-amyloid
236	12	100.0	309	12	100.0	751	22	AAE10649	Human amyloid prot
237	12	100.0	310	12	100.0	751	22	AAE06894	Human amyloid prec
238	12	100.0	311	12	100.0	751	22	AAU06623	Human partial Amyl
239	12	100.0	312	12	100.0	751	22	AAE02601	Human amyloid prec
240	12	100.0	313	12	100.0	753	22	AAE10651	Human amyloid prot
241	12	100.0	314	12	100.0	753	22	AAE06896	Human amyloid prec
242	12	100.0	315	12	100.0	753	22	AAU06625	Human amyloid prec
243	12	100.0	316	12	100.0	753	22	AAU07224	Human amyloid prec
244	12	100.0	317	12	100.0	753	22	AAE02603	Human beta-amyloid
245	12	100.0	318	12	100.0	754	13	AAE26339	APP751. Homo sapi
246	12	100.0	319	12	100.0	754	20	AAW96210	Amyloid precursor
247	12	100.0	320	12	100.0	770	10	AAW94775	Novel amyloid prec
248	12	100.0	321	12	100.0	770	11	AAW05717	NAP gene product a
249	12	100.0	322	12	100.0	770	13	AAE26340	APP770. Homo sapi
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251	12	100.0	324	12	100.0	770	15	AAE63442	Amyloid protein pr
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258	12	100.0	331	12	100.0	770	18	AAW19491	APP770 mutant A-be
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262	12	100.0	335	12	100.0	770	20	AAW97996	Human amyloid prec
263	12	100.0	336	12	100.0	770	22	AAE10648	Human amyloid prot
264	12	100.0	337	12	100.0	770	22	AAE11762	Human amyloid prec
265	12	100.0	338	12	100.0	770	22	AAE06893	Human amyloid prec
266	12	100.0	339	12	100.0	770	22	AAE06912	Human amyloid prec
267	12	100.0	340	12	100.0	770	22	AAE06913	Human amyloid prec
268	12	100.0	341	12	100.0	770	22	AAU06622	Human partial Amyl
269	12	100.0	342	12	100.0	772	22	ABG19086	Human amyloid prec
270	12	100.0	343	12	100.0	772	22	ABG19088	Novel human diago
271	12	100.0	344	12	100.0	772	22	AAE10650	Human amyloid prot
272	12	100.0	345	12	100.0	772	22	AAE06895	Human amyloid prec
273	12	100.0	346	12	100.0	772	22	AAU06624	Human Amyloid prec
274	12	100.0	347	12	100.0	772	22	AAU07223	Human beta-amyloid
275	12	100.0	348	12	100.0	772	22	AAE02602	Human amyloid prec
276	12	100.0	349	12	100.0	772	22	ABG19089	Novel human diago
277	12	100.0	350	12	100.0	798	22	ABG19088	Novel human diago
278	12	100.0	351	11	91.7	11	22	AAE11793	Amyloid beta-prote
279	12	100.0	352	11	91.7	11	22	AAE11793	Amyloid beta-prote
280	12	100.0	353	11	91.7	28	22	AAE11793	Human clone DIN B(
281	12	100.0	354	11	91.7	40	21	AAE11793	Beta-APP A-beta fr
282	12	100.0	355	11	91.7	42	22	AAE11793	Partial sequence o
283	12	100.0	356	11	91.7	42	22	AAE11793	Human amyloid prec
284	12	100.0	357	10	83.3	10	22	AAE11793	Human App derived
285	12	100.0	358	10	83.3	10	22	AAE11793	Human App derived
286	12	100.0	359	10	83.3	10	22	AAE11793	Human App derived
287	12	100.0	360	10	83.3	16	21	AAE11793	Human beta-amyloid
288	12	100.0	361	10	83.3	16	21	AAE11793	Human beta-amyloid
289	12	100.0	362	10	83.3	16	22	AAE11793	Amyloid beta-prote
290	12	100.0	363	10	83.3	16	22	AAE11793	Amyloid beta-prote
291	12	100.0	364	10	83.3	17	11	AAE11793	Cerebrovascular be
292	12	100.0	365	10	83.3	20	21	AAE11793	Beta-APP alpha-sec
293	12	100.0	366	10	83.3	20	21	AAE11793	Beta-APP alpha-sec
294	12	100.0	367	10	83.3	20	21	AAE11793	Beta-APP alpha-sec
295	12	100.0	368	10	83.3	20	21	AAE11793	Beta-APP alpha-sec
296	12	100.0	369	10	83.3	20	21	AAE11793	Beta-APP alpha-sec
297	12	100.0	370	10	83.3	24	15	AAE11793	Alzheimer's diseas
298	12	100.0	371	10	83.3	28	8	AAE11793	Sequence of Alzhei
299	12	100.0	372	10	83.3	28	16	AAE11793	A4-P(1-28) a parti
300	12	100.0	373	10	83.3	28	16	AAE11793	Generic beta amylo
301	12	100.0	374	10	83.3	28	22	AAE11793	Amyloid beta-prote
302	12	100.0	375	10	83.3	28	22	AAE11793	Amyloid beta-prote
303	12	100.0	376	10	83.3	28	22	AAE11793	Human clone Eliq B
						97	9	AAE11793	Deduced sequence o

377	10	83.3	97	9	AAP83152	Lambda SM2W3 encod	450	7	58.3	35	22	AAB91803	Amyloid beta-prote
378	10	83.3	97	14	AAR37865	Beta-amyloid prote	451	7	58.3	35	22	AAB91830	Amyloid beta-prote
379	10	83.3	108	9	AAP83154	Plasmid pAPCp118-3	452	7	58.3	43	22	AAB46177	Tetanus toxoid 830
380	10	83.3	108	14	AAR37868	Beta-amyloid-relat	453	7	58.3	43	22	AAB49076	Tetanus toxoid/tetan
381	9	75.0	10	22	AAB46212	Human APP derived	454	7	58.3	44	22	AAB46194	Tetanus toxoid epi
382	9	75.0	10	22	AAB46216	Human APP derived	455	7	58.3	44	22	AAB49090	Amyloid beta/tetan
383	9	75.0	18	16	AAR75596	Unspecified peptid	456	7	58.3	51	22	AAB46195	Tetanus toxoid epi
384	9	75.0	19	12	AAR14135	Brain-derived prot	457	7	58.3	51	22	AAB49091	Amyloid beta/tetan
385	9	75.0	28	22	AAR35592	Human clone E3Q B(458	7	58.3	72	22	AAB46190	Tetanus toxoid epi
386	9	75.0	32	17	AAR40402	Mouse amyloid prec	459	7	58.3	136	22	AAB49089	Amyloid beta tetan
387	9	75.0	40	22	AAB84429	Partial sequence o	460	6	50.0	6	19	AAW70868	Beta-amyloid pepti
388	9	75.0	53	21	AAB79944	Mammalian amyloid	461	6	50.0	10	22	AAW70869	Human APP derived
389	8	66.7	10	22	AAB46211	Human APP derived	462	6	50.0	10	22	AAB46219	Beta-amyloid pepti
390	8	66.7	10	22	AAB46217	Human APP derived	463	6	50.0	13	19	AAW70869	Human secretase SE
391	8	66.7	16	18	AAW08363	Beta-secretase sub	464	6	50.0	21	20	AAW30941	Human clone H6Q B(
392	8	66.7	16	20	AAV33757	Beta-amyloid prote	465	6	50.0	28	22	AAB35594	Human clone D7Q B(
393	8	66.7	16	21	AAB06315	Human beta-amyloid	466	6	50.0	28	22	AAB35595	Human Receptor to
394	8	66.7	16	21	AAB06316	Human beta-amyloid	467	6	50.0	39	21	AAV52132	Drosophila melanog
395	8	66.7	18	22	AAE00608	Beta-amyloid precu	468	6	50.0	279	22	ABB58516	Arabidopsis thalia
396	8	66.7	18	22	AAE00609	Beta-amyloid precu	469	6	50.0	412	21	AAG22258	Arabidopsis thalia
397	8	66.7	19	22	AAE00611	Amyloid precursor	470	6	50.0	412	21	AAG22258	Arabidopsis thalia
398	8	66.7	19	22	AAE00613	pCBG1 APP beta-sec	471	6	50.0	432	22	AAB73613	Bacillus sp. KSM-K
399	8	66.7	19	22	AAE00614	pCBG1 APP beta-sec	472	6	50.0	432	22	AAB73613	Arabidopsis thalia
400	8	66.7	30	22	AAB47267	Peptide for used i	473	6	50.0	447	21	AAG22257	Arabidopsis thalia
401	8	66.7	45	18	AAW26512	Amyloid precursor	474	6	50.0	447	21	AAG45635	Senescence-induced
402	8	66.7	45	18	AAW26392	Amyloid precursor	475	6	50.0	448	21	AAV97307	Arabidopsis thalia
403	8	66.7	45	19	AAW44748	APP-REP 751 [BAP d	476	6	50.0	529	21	AAG22256	Arabidopsis thalia
404	8	66.7	45	19	AAW44748	Deletion beta-amy	477	5	41.7	5	21	AAG45634	Arabidopsis thalia
405	8	66.7	261	22	AAE00610	Chimeric cassette	478	5	41.7	5	21	AAE10667	Beta-APP alpha-sec
406	7	58.3	8	19	AAW70865	Human APP A-beta p	479	5	41.7	5	22	AAE06907	Human APP-Sw mutan
407	7	58.3	10	22	AAB46210	Beta-amyloid pepti	480	5	41.7	5	22	AAU06636	Human Asp-2 beta-s
408	7	58.3	10	22	AAB46218	Human APP derived	481	5	41.7	5	22	AAU07235	Peptide product of
409	7	58.3	15	17	AAW02333	Human APP derived	482	5	41.7	6	14	AAW32016	Human beta-amyloid
410	7	58.3	15	17	AAW05384	Human APP derived	483	5	41.7	6	19	AAW70864	LAMP-3 lysosome ta
411	7	58.3	15	20	AAW89353	Beta-amyloid pepti	484	5	41.7	6	22	AAB46199	Beta-amyloid pepti
412	7	58.3	15	20	AAE00612	pCBG1 APP beta-sec	485	5	41.7	6	22	AAB49095	Human APP A-beta 1
413	7	58.3	15	20	AAE00612	Tetanus toxoid epi	486	5	41.7	8	18	AAW19494	Immunogen for rais
414	7	58.3	20	22	AAB46179	Tetanus toxoid epi	487	5	41.7	8	18	AAW19507	Human amyloidoid pr
415	7	58.3	20	22	AAB46182	Human APP A-beta 1	488	5	41.7	10	13	AAW42426	Human amyloidoid pr
416	7	58.3	20	22	AAB49078	Amyloid beta/PADRE	489	5	41.7	10	13	AAW42426	Human amyloidoid pr
417	7	58.3	20	22	AAB49081	Amyloid beta/PADRE	490	5	41.7	10	13	AAW42426	Human amyloidoid pr
418	7	58.3	20	22	AAB49081	Unspecified peptid	491	5	41.7	10	13	AAW42426	Beta-secretase sub
419	7	58.3	21	16	AAR75697	Tetanus toxoid 830	492	5	41.7	10	18	AAW08362	Synthetic oligopep
420	7	58.3	21	22	AAB46175	Tetanus toxoid epi	493	5	41.7	10	21	AAV33756	Doubly phosphoryla
421	7	58.3	22	22	AAB46178	Human APP A-beta 1	494	5	41.7	10	21	AAV33756	p-I kappa-B-alpha
422	7	58.3	22	22	AAB46196	Tetanus toxoid epi	495	5	41.7	10	21	AAV96712	Beta-APP alpha-sec
423	7	58.3	22	22	AAB46203	Tetanus toxoid epi	496	5	41.7	10	21	AAV96719	Beta-APP alpha-sec
424	7	58.3	24	22	AAB46183	Tetanus toxoid epi	497	5	41.7	10	21	AAV69703	Beta-APP alpha-sec
425	7	58.3	24	22	AAB46184	Tetanus toxoid epi	498	5	41.7	10	21	AAV69704	Beta-APP alpha-sec
426	7	58.3	24	22	AAB46185	Tetanus toxoid epi	499	5	41.7	10	21	AAV69705	Beta-APP alpha-sec
427	7	58.3	24	22	AAB49082	Amyloid beta/haema	500	5	41.7	10	21	AAV69706	Beta-APP alpha-sec
428	7	58.3	24	22	AAB49083	Amyloid beta/haema	501	5	41.7	10	21	AAV69707	Beta-APP alpha-sec
429	7	58.3	24	22	AAB49084	Amyloid beta/tetan	502	5	41.7	10	21	AAV69708	Beta-APP alpha-sec
430	7	58.3	25	22	AAB49092	Tetanus toxoid epi	503	5	41.7	10	21	AAV69709	Beta-APP alpha-sec
431	7	58.3	27	22	AAB46187	Tetanus toxoid epi	504	5	41.7	10	21	AAV69710	Human APP-Sw beta-
432	7	58.3	27	22	AAB46189	Amyloid beta/tetan	505	5	41.7	10	22	AAE10653	Human wild-type AP
433	7	58.3	27	22	AAB49074	Amyloid beta/tetan	506	5	41.7	10	22	AAE10654	Human amyloid prec
434	7	58.3	27	22	AAB49077	Amyloid beta/haema	507	5	41.7	10	22	AAE06899	Human amyloid prec
435	7	58.3	27	22	AAB49086	Amyloid beta/haema	508	5	41.7	10	22	AAU06827	Synthetic Asp2 rec
436	7	58.3	27	22	AAB49088	Tetanus toxoid 947	509	5	41.7	10	22	AAU06628	Human beta-amyloid
437	7	58.3	28	22	AAB46176	Tetanus toxoid 947	510	5	41.7	10	22	AAU07226	Human beta-amyloid
438	7	58.3	28	22	AAB35593	Human clone R5Q B(511	5	41.7	10	22	AAU07227	Human wild-type AP
439	7	58.3	32	17	AAW04403	Mouse amyloid prec	512	5	41.7	10	22	AAE02605	Human amyloid prec
440	7	58.3	33	22	AAB49075	Amyloid beta/tetan	513	5	41.7	10	22	AAE02606	Peptide 5-5'SW, fo
441	7	58.3	33	22	AAB46180	Tetanus toxoid epi	514	5	41.7	10	22	AAB47266	Synthetic peptide
442	7	58.3	34	22	AAB46181	Tetanus toxoid epi	515	5	41.7	10	22	AAB66574	Synthetic peptide
443	7	58.3	34	22	AAB46186	Tetanus toxoid epi	516	5	41.7	10	22	AAB66575	Human APP derived
444	7	58.3	34	22	AAB46188	Tetanus toxoid epi	517	5	41.7	10	22	AAB46208	Human APP derived
445	7	58.3	34	22	AAB49079	Amyloid beta/PADRE	518	5	41.7	10	22	AAB46220	Synthetic peptide f
446	7	58.3	34	22	AAB49080	Amyloid beta/haema	519	5	41.7	10	22	AAB61336	Synthetic peptide f
447	7	58.3	34	22	AAB49085	Amyloid beta/haema	520	5	41.7	10	22	AAB61337	Swedish mutation p
448	7	58.3	34	22	AAB49087	Beta-amyloid pepti	521	5	41.7	10	22	AAB61337	Swedish mutation p
449	7	58.3	35	20	AAW89357	Beta-amyloid pepti	522	5	41.7	11	22	AAW75142	Swedish mutation p

523	5	41.7	11	22	AAB75143	APP beta-secretase	596	5	41.7	272	20	AAV35667	C. pneumoniae prot
524	5	41.7	11	22	AAB75144	Asp 1 substrate se	597	5	41.7	279	22	AAU68012	Propionibacterium
525	5	41.7	11	22	AAB75145	Asp 1 substrate se	598	5	41.7	280	18	AAW29265	Human inhibitory k
526	5	41.7	11	22	AAB97468	Asp2 substrate wil	599	5	41.7	280	22	ABBS8639	Drosophila melanog
527	5	41.7	11	22	AAB97469	Asp2 substrate Swe	600	5	41.7	281	22	ABG48012	Arabidopsis thalia
528	5	41.7	12	19	AAW59831	Human I-kappa-B mo	601	5	41.7	284	22	ABB66010	Drosophila melanog
529	5	41.7	12	21	AAV96701	Doubly phosphoryla	602	5	41.7	286	22	AAU47562	Propionibacterium
530	5	41.7	12	22	AAAB6334	Indole-derivative	603	5	41.7	289	18	AAW29264	Human inhibitory k
531	5	41.7	16	19	AAW59832	Human I-kappa-B mo	604	5	41.7	300	17	AAV99959	B.t.t. coleopteran
532	5	41.7	16	21	AAV96702	Doubly phosphoryla	605	5	41.7	303	17	AAW88642	Human protein C wh
533	5	41.7	20	19	AAW59833	Human I-kappa-B mo	606	5	41.7	308	22	AAW88642	C glutamicum prote
534	5	41.7	20	21	AAV96703	Doubly phosphoryla	607	5	41.7	310	22	ABG10520	Novel human diago
535	5	41.7	21	21	AAAB20842	Ikbalpha ubiquitin	608	5	41.7	314	15	AAW54664	I kappa B like pro
536	5	41.7	21	21	AAV54016	Phosphoserine cont	609	5	41.7	314	19	AAW79131	Murine IkappaB pol
537	5	41.7	21	22	AAV508050	Peptide of IxB. U	610	5	41.7	316	19	AAW79132	Human IkappaB poly
538	5	41.7	22	19	AAW59834	Human I-kappa-B mo	611	5	41.7	317	13	AAW29577	IKB NP-kappa-B-bin
539	5	41.7	22	19	AAW56330	Synthetic peptide	612	5	41.7	317	18	AAW29262	Human inhibitory k
540	5	41.7	22	21	AAW20855	Ubiquitination rec	613	5	41.7	317	19	AAW59828	Human I-kappa-B-al
541	5	41.7	22	21	AAV96704	I-kappa-B-alpha pe	614	5	41.7	317	19	AAW56324	Amino acid sequenc
542	5	41.7	23	22	AAB75147	Asp 1 substrate se	615	5	41.7	317	20	AAV25171	Human MAD3 protein
543	5	41.7	23	22	AAB75148	Asp 1 substrate se	616	5	41.7	317	21	AAV96698	Human I-kappa-B-al
544	5	41.7	23	22	AAB97473	Asp2 substrate wil	617	5	41.7	317	22	AAG75055	Human colon cancer
545	5	41.7	23	22	AAB97474	Asp2 substrate Swe	618	5	41.7	325	22	AAG91087	C glutamicum prote
546	5	41.7	27	22	AAW52235	I kappa B (15-41)	619	5	41.7	325	22	AAW91087	Corynebacterium gl
547	5	41.7	31	22	AAW36778	Peptide #10815 enc	620	5	41.7	327	22	AAW91087	Human protein SEQ
548	5	41.7	35	20	AAW89361	Beta-amyloid pepti	621	5	41.7	327	22	AAW41005	Human polypeptide
549	5	41.7	56	22	AAU91443	Human immune/haema	622	5	41.7	332	21	AAW91087	Arabidopsis thalia
550	5	41.7	68	22	AAU56631	Propionibacterium	623	5	41.7	332	21	AAW91087	Arabidopsis thalia
551	5	41.7	70	22	AAU49777	Propionibacterium	624	5	41.7	337	21	AAW91087	Arabidopsis thalia
552	5	41.7	72	21	AAW55847	Arabidopsis thalia	625	5	41.7	342	21	AAW91087	Arabidopsis thalia
553	5	41.7	72	21	AAW58892	Arabidopsis thalia	626	5	41.7	342	21	AAW91087	HA-tagged I-kappa-
554	5	41.7	82	22	AAU56643	Propionibacterium	627	5	41.7	347	21	AAW91087	Micromonospora eve
555	5	41.7	84	22	AAU58355	Propionibacterium	628	5	41.7	351	22	AAU04828	C glutamicum prote
556	5	41.7	88	22	AAU45537	Human polypeptide	629	5	41.7	352	22	AAW91087	Helicobacter pylor
557	5	41.7	88	22	AAU09855	Novel human respir	630	5	41.7	355	21	AAW91087	Mouse Stat1 protei
558	5	41.7	91	22	AAU17842	Propionibacterium	631	5	41.7	356	21	AAW91087	Ehrlichia sp. exte
559	5	41.7	103	22	AAU60926	Novel human respir	632	5	41.7	372	21	AAW91087	Drosophila melanog
560	5	41.7	107	22	AAW60926	Novel human respir	633	5	41.7	376	22	AAW91087	Putative P. abyss
561	5	41.7	110	17	AAW03165	Propionibacterium	634	5	41.7	378	19	AAW91087	Human normal ovar
562	5	41.7	112	22	AAU60798	Drosophila melanog	635	5	41.7	378	21	AAW91087	Human novel protei
563	5	41.7	116	22	AAU60798	Human STAT1 DNA bi	636	5	41.7	398	22	AAW91087	Drosophila melanog
564	5	41.7	120	22	AAU35562	Novel human diago	637	5	41.7	406	22	AAW91087	Drosophila G-prote
565	5	41.7	120	22	AAU35562	Novel human diago	638	5	41.7	412	22	AAW91087	Protaminobacter ru
566	5	41.7	120	22	AAU35562	Chlamydia pneumoni	639	5	41.7	412	22	AAW91087	Drosophila melanog
567	5	41.7	120	22	AAW58321	Novel human diago	640	5	41.7	412	22	AAW91087	Drosophila melanog
568	5	41.7	120	22	AAW18632	Human brain expres	641	5	41.7	432	22	AAW91087	E. raphontici palh
569	5	41.7	120	22	AAW06198	Peptide #5066 enco	642	5	41.7	432	22	AAW91087	H. pylori ORF 07ee
570	5	41.7	134	22	AAU15306	Peptide #4880 enco	643	5	41.7	432	22	AAW91087	Escherichia coli p
571	5	41.7	141	22	AAU50269	Novel human diago	644	5	41.7	432	22	AAW91087	Moraxella catarrha
572	5	41.7	160	22	AAU0753	Novel human diago	645	5	41.7	432	22	AAW91087	Moraxella catarrha
573	5	41.7	163	22	AAW67354	Human polypeptide	646	5	41.7	432	22	AAW91087	Moraxella catarrha
574	5	41.7	171	22	AAW19969	Drosophila melanog	647	5	41.7	432	22	AAW91087	Moraxella catarrha
575	5	41.7	176	22	AAW07745	Human STAT-1 DNA b	648	5	41.7	432	22	AAW91087	Pseudomonas aerugi
576	5	41.7	181	22	AAW20089	Novel human diago	649	5	41.7	432	22	AAW91087	Amino acid sequenc
577	5	41.7	183	22	AAW91737	Novel human diago	650	5	41.7	432	22	AAW91087	Human protein sequ
578	5	41.7	194	22	AAW23890	C glutamicum prote	651	5	41.7	432	22	AAW91087	Drosophila melanog
579	5	41.7	195	22	AAW09785	Novel human diago	652	5	41.7	432	22	AAW91087	Human adrenorecept
580	5	41.7	198	22	AAW69525	Arabidopsis thalia	653	5	41.7	432	22	AAW91087	Sequence of HuAlph
581	5	41.7	199	22	AAW99982	Drosophila thalia	654	5	41.7	432	22	AAW91087	Alpha lb adrenergi
582	5	41.7	199	22	AAW99982	Human polypeptide,	655	5	41.7	432	22	AAW91087	Sequence of human
583	5	41.7	204	22	AAW82062	C glutamicum prote	656	5	41.7	432	22	AAW91087	Alpha-lb adrenergi
584	5	41.7	204	22	AAW82062	Arabidopsis thalia	657	5	41.7	432	22	AAW91087	Human alpha-lb adr
585	5	41.7	213	21	AAW09785	Arabidopsis thalia	658	5	41.7	432	22	AAW91087	Partial human DNAX
586	5	41.7	215	22	AAW14661	Human inhibitory k	659	5	41.7	432	22	AAW91087	Human polypeptide,
587	5	41.7	218	22	AAW93514	Arabidopsis thalia	660	5	41.7	432	22	AAW91087	Drosophila melanog
588	5	41.7	218	22	AAW93514	Human polypeptide,	661	5	41.7	432	22	AAW91087	GFP-I-kappa-B fusi
589	5	41.7	222	21	AAW09784	C glutamicum prote	662	5	41.7	432	22	AAW91087	Human protein SEQ
590	5	41.7	228	21	AAW08601	Arabidopsis thalia	663	5	41.7	432	22	AAW91087	Pseudorabies virus
591	5	41.7	242	18	AAW29267	Arabidopsis thalia	664	5	41.7	432	22	AAW91087	Glycoprotein I(gpI
592	5	41.7	249	21	AAW06540	Human inhibitory k	665	5	41.7	432	22	AAW91087	
593	5	41.7	258	21	AAW14660	Arabidopsis thalia	666	5	41.7	432	22	AAW91087	
594	5	41.7	258	21	AAW14660	Arabidopsis thalia	667	5	41.7	432	22	AAW91087	
595	5	41.7	258	21	AAW31757	Arabidopsis thalia	668	5	41.7	432	22	AAW91087	
596	5	41.7	266	18	AAW29266	Human inhibitory k	669	5	41.7	432	22	AAW91087	

669	5	41.7	577	21	AAB10096	Swine pseudorabies	742	5	41.7	19	AAW62995	Human Stat1-beta p
670	5	41.7	577	22	AAE05397	pseudorabies virus	743	5	41.7	712	AAW70451	Human membrane cha
671	5	41.7	577	22	AAU04971	Pseudorabies virus	744	5	41.7	724	ABE58970	Drosophila melanog
672	5	41.7	577	22	AAW82503	pseudorabies virus	745	5	41.7	738	AAU41334	91 kD ISGF-3alpha
673	5	41.7	582	19	AAW82596	Human truncated St	746	5	41.7	739	AAW72078	Human Stat91. Hom
674	5	41.7	592	22	AAW79939	Human protein SEQ	747	5	41.7	750	AAW03168	Human Stat1-alpha
675	5	41.7	597	17	AAW00334	Bacillus thuringie	748	5	41.7	750	AAW62994	Human Stat1-alpha
676	5	41.7	597	22	AAW69666	Wild-type Bacillus	749	5	41.7	750	AAW19962	Human signal trans
677	5	41.7	604	21	AAW65271	Cell factor recept	750	5	41.7	786	AAW54098	Human pancreatic c
678	5	41.7	609	22	AAU38090	Streptococcus pneu	751	5	41.7	795	AAU46066	Propionibacterium
679	5	41.7	610	11	AAW05537	Synthetic Bacillus	752	5	41.7	838	ABW58132	Drosophila melanog
680	5	41.7	610	16	AAW85482	Btc synthetic (72A	753	5	41.7	866	AAW35864	Arabidopsis thalia
681	5	41.7	610	17	AAW00333	Bacillus thuringie	754	5	41.7	873	AAW68207	Arabidopsis thalia
682	5	41.7	610	21	AAW69667	Bacillus thuringie	755	5	41.7	874	AAW35863	Arabidopsis thalia
683	5	41.7	619	22	AAW64953	Human ATP-dependen	756	5	41.7	887	AAW35862	B.thuringiensis to
684	5	41.7	626	22	AAU14731	Novel bone marrow	757	5	41.7	914	AAW15785	Drosophila melanog
685	5	41.7	636	19	AAW333399	Alternatively spli	758	5	41.7	950	ABW71513	B.thuringiensis to
686	5	41.7	636	20	AAW29781	Human DNAX cytokin	759	5	41.7	956	AAW15784	Drosophila melanog
687	5	41.7	636	22	AAW65270	Cell factor recept	760	5	41.7	1066	ABW64251	B.thuringiensis to
688	5	41.7	636	22	AAU01853	Sequence of toxin	761	5	41.7	1100	AAW15783	Drosophila melanog
689	5	41.7	644	8	AAW00085	Bacillus thuringie	762	5	41.7	1114	ABW71505	Drosophila melanog
690	5	41.7	644	9	AAW80467	Delta endotoxin en	763	5	41.7	1236	ABW71384	Amino acid sequenc
691	5	41.7	644	9	AAW82487	Amino acid sequenc	764	5	41.7	1288	AAW67880	Retinoblastoma bin
692	5	41.7	644	10	AAW94679	M-7 crystal toxin.	765	5	41.7	1312	AAW76884	Human transcriptio
693	5	41.7	644	10	AAW95585	Delta endotoxin.	766	5	41.7	1312	ABW50244	Human polypeptide
694	5	41.7	644	14	AAW39751	CryIIIA insecticida	767	5	41.7	1312	ABW38967	Amino acid sequenc
695	5	41.7	644	15	AAW56697	CryIIB insecticida	768	5	41.7	1378	AAW67879	Human receptor tyr
696	5	41.7	644	15	AAW56698	Bacillus thuringie	769	5	41.7	1503	AAW48845	Drosophila melanog
697	5	41.7	644	17	AAW99958	B.t.t. coleopteran	770	5	41.7	1519	AAW66635	Drosophila melanog
698	5	41.7	644	17	AAW99960	Novel CryIIIA muta	771	5	41.7	1767	ABW62726	Drosophila melanog
699	5	41.7	644	18	AAW34811	Novel CryIIIA muta	772	5	41.7	1963	ABW62819	Novel human diagno
700	5	41.7	644	18	AAW34812	Novel CryIIIA muta	773	5	41.7	2506	ABG07191	Novel human diagno
701	5	41.7	644	18	AAW34813	Novel CryIIIA muta	774	5	41.7	2506	ABG30064	Virulence gene clu
702	5	41.7	644	18	AAW34814	Novel CryIIIA muta	775	5	41.7	4472	AAW97245	Drosophila melanog
703	5	41.7	644	18	AAW34815	Novel CryIIIA muta	776	5	41.7	4472	ABW60101	Beta-amyloid pepti
704	5	41.7	644	18	AAW34816	Novel CryIIIA muta	777	4	33.3	4	AAW70870	b-secretase substr
705	5	41.7	644	18	AAW34817	Novel CryIIIA muta	778	4	33.3	4	AAW22905	Beta-amyloid prote
706	5	41.7	644	18	AAW34818	Novel CryIIIA muta	779	4	33.3	4	AAW79607	Human NSE promoter
707	5	41.7	644	18	AAW34819	Novel CryIIIA muta	780	4	33.3	5	AAW37864	Sphingolipid desat
708	5	41.7	644	18	AAW34820	Novel CryIIIA muta	781	4	33.3	5	AAW08608	Epitope pattern #
709	5	41.7	644	18	AAW34821	Novel CryIIIA muta	782	4	33.3	5	AAW51336	Epitope #1 used in
710	5	41.7	644	18	AAW34822	Novel CryIIIA muta	783	4	33.3	6	AAW06998	Antimalarial pepti
711	5	41.7	644	18	AAW34823	Novel CryIIIA muta	784	4	33.3	6	AAW47109	Antimalarial pepti
712	5	41.7	644	18	AAW34824	Novel CryIIIA muta	785	4	33.3	7	AAW27256	Mammalian ribonuc
713	5	41.7	644	18	AAW34825	Novel CryIIIA muta	786	4	33.3	7	AAW27258	Peptide derived fr
714	5	41.7	644	18	AAW34826	Novel CryIIIA muta	787	4	33.3	7	AAW72756	Nucleotide-binding
715	5	41.7	644	18	AAW34827	Novel CryIIIA muta	788	4	33.3	7	AAW07656	Ribonucleotide red
716	5	41.7	644	18	AAW34828	Novel CryIIIA muta	789	4	33.3	7	AAW02941	Molecular mimetic
717	5	41.7	644	18	AAW34829	Novel CryIIIA muta	790	4	33.3	7	AAW83859	Humanised ATR-5 H
718	5	41.7	644	18	AAW34830	Novel CryIIIA muta	791	4	33.3	8	AAW57516	Beta-secretase sub
719	5	41.7	644	18	AAW34831	Novel CryIIIA muta	792	4	33.3	8	AAW52751	Beta-secretase sub
720	5	41.7	644	18	AAW34832	Novel CryIIIA muta	793	4	33.3	8	AAW94771	Beta-secretase sub
721	5	41.7	644	18	AAW34833	Novel CryIIIA muta	794	4	33.3	8	AAW94772	Beta-secretase sub
722	5	41.7	644	18	AAW34834	Novel CryIIIA muta	795	4	33.3	8	AAW94773	Human Aspartyl pro
723	5	41.7	644	18	AAW34835	Novel CryIIIA muta	796	4	33.3	8	AAE10660	Human aspartyl pro
724	5	41.7	644	18	AAW34836	Novel CryIIIA muta	797	4	33.3	8	AAE10661	Human amyloid prec
725	5	41.7	644	18	AAW34837	Novel CryIIIA muta	798	4	33.3	8	AAE06902	Beta secretase sub
726	5	41.7	644	18	AAW34838	Novel CryIIIA muta	799	4	33.3	8	AAU06631	Synthetic fluoresc
727	5	41.7	644	18	AAW34839	Novel CryIIIA muta	800	4	33.3	8	AAU06635	Human beta-amyloid
728	5	41.7	644	18	AAW34840	Novel CryIIIA muta	801	4	33.3	8	AAU07230	Human Aspartyl pro
729	5	41.7	644	18	AAW34841	Novel CryIIIA muta	802	4	33.3	8	AAE02612	Human Aspartyl pro
730	5	41.7	644	22	AAW84195	Amino acid sequenc	803	4	33.3	8	AAE02612	Tyrosine-kinase in
731	5	41.7	645	18	AAW34784	An artificial modi	804	4	33.3	9	AAW55719	Fluorogenic protea
732	5	41.7	646	22	AAW64598	Drosophila melanog	805	4	33.3	9	AAW82081	Fluorogenic protea
733	5	41.7	649	12	AAW15630	Btl109p insecticid	806	4	33.3	9	AAW82082	Fluorogenic protea
734	5	41.7	652	20	AAW23214	Amino acid sequenc	807	4	33.3	9	AAW82083	A peptide fragment
735	5	41.7	652	20	AAW23217	Amino acid sequenc	808	4	33.3	9	AAW07873	A peptide fragment
736	5	41.7	663	22	ABW64497	Drosophila melanog	809	4	33.3	9	AAW07874	A peptide fragment
737	5	41.7	680	22	ABG30166	Novel human diagno	810	4	33.3	9	AAW07875	A peptide fragment
738	5	41.7	683	22	ABW11820	Human secreted pro	811	4	33.3	9	AAW07876	A peptide fragment
739	5	41.7	701	14	AAW41335	84 kD ISGF-3alpha	812	4	33.3	9	AAW07877	Substrate for beta
740	5	41.7	712	16	AAW72079	Human Stat84. Hom	813	4	33.3	9	AAW07894	Mammalian amyloid
741	5	41.7	712	17	AAW03170	Human STAT1-beta.	814	4	33.3	9	AAW87949	

815	4	33.3	9	21	AAV51340	Sphingolipid desat	888	4	33.3	24	19	AAW71985	Dermatophagoides D
816	4	33.3	9	22	AAU02736	CDR region of anti	889	4	33.3	24	20	AAV50439	Dermatophagoides s
817	4	33.3	9	22	AAU02741	CDR region of anti	890	4	33.3	24	22	AAU19042	T-cell epitope con
818	4	33.3	9	22	AGG73279	Protease indicator	891	4	33.3	26	14	AAK36463	Der f I (197-222), a
819	4	33.3	9	22	AGG73280	Protease indicator	892	4	33.3	26	15	AAK51811	Der f I derived pe
820	4	33.3	9	22	AGG73293	Protease indicator	893	4	33.3	26	19	AAW71986	Dermatophagoides D
821	4	33.3	9	22	AGG73297	Protease indicator	894	4	33.3	26	20	AAV50440	Dermatophagoides s
822	4	33.3	10	11	AAU08279	Laminin receptor-b	895	4	33.3	26	22	AAU19043	Protease binding s
823	4	33.3	10	13	AAU22054	Peptide Pl. Synth	896	4	33.3	26	22	AAU19043	T-cell epitope con
824	4	33.3	10	13	AAU24266	Human amyloidin pr	897	4	33.3	27	14	AAU0079	Hib OMP P2 peptide
825	4	33.3	10	17	AAW12588	SH2 binding peptid	898	4	33.3	28	20	AAU02578	Fragment of human
826	4	33.3	10	18	AAW36714	Thrombopoietin rec	899	4	33.3	29	14	AAK36475	Der f I derived pe
827	4	33.3	10	18	AAW09563	Thrombopoietin rec	900	4	33.3	29	15	AAK36475	Betal-alpha-beta2
828	4	33.3	10	20	AAW82440	Human amyloid beta	901	4	33.3	29	17	AAW08431	Dermatophagoides D
829	4	33.3	10	21	AAV69711	Beta-APP alpha-sec	902	4	33.3	29	19	AAW71997	Dermatophagoides s
830	4	33.3	10	21	AAV69712	Beta-APP alpha-sec	903	4	33.3	29	20	AAV50452	T-cell epitope con
831	4	33.3	10	22	AAU25913	Human thrombopoiet	904	4	33.3	29	22	AAU19055	Beta-secretase sub
832	4	33.3	10	22	AAW43151	Mycoplasma genital	905	4	33.3	30	18	AAW08360	Synthetic oligopep
833	4	33.3	10	22	AAW43153	Mycoplasma genital	906	4	33.3	30	20	AAV33754	HCV-1b variant ISD
834	4	33.3	10	22	AAW43155	Beta-sheet breaker	907	4	33.3	30	21	AAU2814	Peptide #6376 enco
835	4	33.3	10	22	AAW43155	Human complementar	908	4	33.3	30	21	AAU07895	Protein #5873 enco
836	4	33.3	10	22	AAW43155	Human complementar	909	4	33.3	30	22	ABB38870	Human brain expres
837	4	33.3	10	22	AAW43155	Peptide #3 used in	910	4	33.3	30	22	AAU59517	Human bone marrow
838	4	33.3	10	22	AAW43155	Human APP derived	911	4	33.3	30	22	AAU59517	Peptide #5863 enco
839	4	33.3	10	22	AAW43155	Human APP derived	912	4	33.3	30	22	AAU59517	Peptide #6382 enco
840	4	33.3	10	22	AAW43155	IL-6R-derived back	913	4	33.3	30	22	AAU59517	Peptide 26-4'SW, f
841	4	33.3	10	22	AAW43155	Linker peptide ami	914	4	33.3	30	22	AAU59517	Peptide encoded by
842	4	33.3	11	21	AAU02663	CDR region of anti	915	4	33.3	31	22	AAU59517	Human bone marrow
843	4	33.3	11	21	AAU02663	CDR region of anti	916	4	33.3	31	22	AAU59517	Peptide #7677 enco
844	4	33.3	12	21	AAU39745	Anti-IL12 antibody	917	4	33.3	31	22	AAU59517	Human bone marrow
845	4	33.3	12	21	AAU39745	Beta-amyloid precu	918	4	33.3	31	22	AAU59517	Peptide #7857 enco
846	4	33.3	13	7	AAU61425	Sequence of linear	919	4	33.3	31	22	AAU59517	Mouse amyloid prec
847	4	33.3	13	7	AAU61425	Anti-FIX/FIXa anti	920	4	33.3	32	17	AAU04401	Mouse amyloid prec
848	4	33.3	13	7	AAU61425	Peptide derived fr	921	4	33.3	32	17	AAU04401	Substrate for beta
849	4	33.3	13	7	AAU61425	Peptide derived fr	922	4	33.3	32	17	AAU04401	Hepatitis C virus
850	4	33.3	13	7	AAU61425	Human SNP related	923	4	33.3	32	17	AAU04401	Arabidopsis thalia
851	4	33.3	14	22	ABB56899	Mutant sequence of	924	4	33.3	34	21	AAU04401	Peptide #2360 enco
852	4	33.3	15	20	AAV30467	Mutant sequence of	925	4	33.3	35	22	AAU04401	Peptide #2295 enco
853	4	33.3	15	20	AAV30467	Quenched fluoresce	926	4	33.3	35	22	AAU04401	Protein encoded by
854	4	33.3	15	20	AAV30467	MRP signature sequ	927	4	33.3	36	22	AAU04401	TSAR C46-9-1 pepti
855	4	33.3	15	20	AAV30467	Human Asp-2b activ	928	4	33.3	36	22	AAU04401	Human nervous syst
856	4	33.3	15	20	AAV30467	Human beta-amyloid	929	4	33.3	37	22	AAU04401	Human reproductive
857	4	33.3	15	20	AAV30467	Epitope #2 used in	930	4	33.3	37	22	AAU04401	Human digestive sy
858	4	33.3	15	20	AAV30467	EFRH containing pe	931	4	33.3	37	22	AAU04401	TSAR GAM-9-4 pepti
859	4	33.3	15	20	AAV30467	EFRH containing pe	932	4	33.3	38	15	AAU04401	Amino acid sequenc
860	4	33.3	16	19	AAU71117	Human neuroendocri	933	4	33.3	38	18	AAU04401	Human secreted pro
861	4	33.3	17	18	AAU71117	Beta-amyloid pepti	934	4	33.3	39	15	AAU04401	Invertebrate neuro
862	4	33.3	17	18	AAU71117	Complementary dete	935	4	33.3	39	15	AAU04401	N-terminal of M.ka
863	4	33.3	17	18	AAU71117	Staphylokinase min	936	4	33.3	39	15	AAU04401	HCV interferon sen
864	4	33.3	18	16	AAU71117	N-terminal 39 kDa	937	4	33.3	39	18	AAU04401	HCV-1b ISD core re
865	4	33.3	18	16	AAU71117	Anti-FIX/FIXa anti	938	4	33.3	39	18	AAU04401	HCV-1b variant ISD
866	4	33.3	18	16	AAU71117	AEDANS-beta-amyloi	939	4	33.3	39	18	AAU04401	HCV-1b variant ISD
867	4	33.3	19	18	AAU71117	Trp-Beta-amyloid p	940	4	33.3	39	22	AAU04401	HCV-1b variant ISD
868	4	33.3	20	19	AAU71117	Fluorogenic protea	941	4	33.3	39	22	AAU04401	HCV-1b variant ISD
869	4	33.3	20	19	AAU71117	Protease binding s	942	4	33.3	39	22	AAU04401	HCV-1b variant ISD
870	4	33.3	20	22	AAU71117	Protease binding s	943	4	33.3	39	22	AAU04401	HCV-1b variant ISD
871	4	33.3	20	22	AAU71117	Protease binding s	944	4	33.3	39	22	AAU04401	HCV-1b variant ISD
872	4	33.3	20	22	AAU71117	Protease binding s	945	4	33.3	40	5	AAU04401	Human immune/haema
873	4	33.3	20	22	AAU71117	Protease indicator	946	4	33.3	40	5	AAU04401	Enterovirus 71/BrC
874	4	33.3	20	22	AAU71117	Protease indicator	947	4	33.3	40	5	AAU04401	Enterovirus 71/238
875	4	33.3	21	19	AAU71117	Adrenomedullin pep	948	4	33.3	40	22	AAU04401	Coxsackievirus A16
876	4	33.3	21	19	AAU71117	Fluorogenic protea	949	4	33.3	40	22	AAU04401	Amyloid beta-prote
877	4	33.3	21	19	AAU71117	Fluorogenic protea	950	4	33.3	40	22	AAU04401	Amyloid beta-prote
878	4	33.3	21	19	AAU71117	Fluorogenic protea	951	4	33.3	40	22	AAU04401	Amyloid beta-prote
879	4	33.3	21	22	AAU71117	Protease binding s	952	4	33.3	40	22	AAU04401	GET epitope C Inse
880	4	33.3	21	22	AAU71117	Protease binding s	953	4	33.3	40	22	AAU04401	
881	4	33.3	21	22	AAU71117	Protease binding s	954	4	33.3	40	22	AAU04401	
882	4	33.3	21	22	AAU71117	Protease binding s	955	4	33.3	40	22	AAU04401	
883	4	33.3	21	22	AAU71117	Protease binding s	956	4	33.3	40	22	AAU04401	
884	4	33.3	21	22	AAU71117	Macrophage stimula	957	4	33.3	40	22	AAU04401	
885	4	33.3	22	21	AAU71117	SSAD fragment of f	958	4	33.3	40	22	AAU04401	
886	4	33.3	22	21	AAU71117	Human colon cancer	959	4	33.3	40	22	AAU04401	
887	4	33.3	24	14	AAU71117	DFI-10(181-204), a	960	4	33.3	41	15	AAU71117	
	4	33.3	24	15	AAU71117	Der f I derived pe		4	33.3	41	15	AAU71117	

Fri Sep 13 09:18:10 2002

100.0%; Score 12; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 daefrhdsgyev 12

RESULT 2
AAB49094
ID AAB49094 standard; peptide; 13 AA.
XX
AC AAB49094;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human amyloid beta peptide (residues 1-12), SEQ ID NO:30.
XX
KW Amyloid disease; amyloid fibril deposition; amyloid plaque;
KW immunogenic; antibody; vaccine; Alzheimer's disease;
KW type 2 diabetes; reactive system amyloidosis;
KW systemic senile amyloidosis; familial amyloid cardiomyopathy;
KW transmissible spongiform encephalopathy; Creutzfeldt-Jakob disease; Kuru;
KW haemodialysis-associated beta-2-microglobulin deposition;
KW amyloid beta peptide.
XX
OS Homo sapiens.
XX
PN WO200072876-A2.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15239.
XX
PR 01-JUN-1999; 99US-0137010.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB;
XX
DR WPI; 2001-070921/08.
XX
PT Pharmaceutical composition comprising immunogen against amyloid
PT component such as fibril peptide or protein, or antibody against
PT amyloid component useful for treating amyloid diseases or amyloidoses -
XX
XX Example IV; Page 74; 140pp; English.
PS

ALIGNMENTS

RESULT 1
AAB46198
ID AAB46198 standard; peptide; 13 AA.
XX
AC AAB46198;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP A-beta 1-12 peptide.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX

DR
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Page 61; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have neurotropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 12; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 daefrhdsgyev 12

RESULT 2
AAB49094
ID AAB49094 standard; peptide; 13 AA.
XX
AC AAB49094;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human amyloid beta peptide (residues 1-12), SEQ ID NO:30.
XX
KW Amyloid disease; amyloid fibril deposition; amyloid plaque;
KW immunogenic; antibody; vaccine; Alzheimer's disease;
KW type 2 diabetes; reactive system amyloidosis;
KW systemic senile amyloidosis; familial amyloid cardiomyopathy;
KW transmissible spongiform encephalopathy; Creutzfeldt-Jakob disease; Kuru;
KW haemodialysis-associated beta-2-microglobulin deposition;
KW amyloid beta peptide.
XX
OS Homo sapiens.
XX
PN WO200072876-A2.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15239.
XX
PR 01-JUN-1999; 99US-0137010.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB;
XX
DR WPI; 2001-070921/08.
XX
PT Pharmaceutical composition comprising immunogen against amyloid
PT component such as fibril peptide or protein, or antibody against
PT amyloid component useful for treating amyloid diseases or amyloidoses -
XX
XX Example IV; Page 74; 140pp; English.
PS

XX The invention relates to a novel pharmaceutical composition for
 CC preventing or treating a disease characterised by amyloid fibril
 CC deposits (amyloid plaques) in a patient. The pharmaceutical composition
 CC comprises an agent that will induce an immune response against an amyloid
 CC component, or an antibody or antibody fragment that binds to an amyloid
 CC component. The invention also relates to a method for determining
 CC the prognosis of a patient undergoing treatment for an amyloid disorder
 CC which involves measuring a patient serum amount of immunoreactivity
 CC against a selected amyloid component. A patient serum immunoreactivity
 CC of at least four times a base line serum immunoreactivity control level
 CC indicates a prognosis of improved status with respect to the disorder.
 CC The pharmaceutical compositions of the invention are useful for treating
 CC a wide variety of disorders characterised by amyloid fibril deposition in
 CC a patient. Such disorders include Alzheimer's disease characterised by
 CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by
 CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
 CC amyloidosis associated with systemic inflammatory diseases (e.g.,
 CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
 CC fibrils derived from serum amyloid A protein (ApoSAA); systemic senile
 CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
 CC fibrils derived from transthyretin (TTR); transmissible spongiform
 CC encephalopathies (e.g. Creutzfeldt-Jakob disease, Kuru) characterised by
 CC prion protein deposits; and beta-2-microglobulin deposits which form as
 CC a result of long term haemodialysis treatment. The present sequence
 CC represents a human amyloid beta peptide which was conjugated to
 CC sheep anti-mouse IgG in an exemplification of the invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 12; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 |||||
 Db 1 daefrhdsgyev 12

RESULT 3

AAW81466
 ID AAW81466 standard; peptide; 15 AA.

AC AAW81466;

DT 28-JAN-1999 (first entry)

DE Synthetic amyloid beta (Abeta) peptide 1 (residues 1-15).

KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 research; neurotoxicity; free-radical; glutamine synthetase.

OS Synthetic.

PN US5840838-A.

PD 24-NOV-1998.

PF 29-FEB-1996; 96US-0609090.

PR 29-FEB-1996; 96US-0609090.

PA (KENT) UNIV KENTUCKY RES FOUND.

PI Aksenov M, Butterfield DA, Carney JM, Hensley K;

DR WPI; 1999-034120/03.

XX Process for treating synthetic amyloid beta peptides - by organic
 PT solvent treatment, useful for studying neurotoxicity

PS Claim 5; Columns 7-8; 14pp; English.

XX

CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
 CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
 CC "evaporative deposition" in 5-10 minutes. Synthetic amyloid beta
 CC peptides are useful as research tools for studying neurotoxicity
 CC resulting from Abeta peptide enhanced free-radical production. The
 CC treatment increases the activity of the synthetic Abeta peptides in tests
 CC to determine free-radical generating capacity and glutamine synthetase
 CC inactivation.

XX Sequence 15 AA;

Query Match 100.0%; Score 12; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 |||||
 Db 1 daefrhdsgyev 12

RESULT 4

AAW60371

ID AAR60371 standard; peptide; 16 AA.

AC AAR60371;

DT 15-MAR-1995 (first entry)

DE Beta-amyloid (1-16).

KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
 anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.

OS Homo sapiens.

PN WO9417197-A.

PD 04-AUG-1994.

PF 24-JAN-1994; 94WO-JP00089.

PR 25-JAN-1993; 93JP-0010132.

PR 05-FEB-1993; 93JP-0019035.

PR 16-NOV-1993; 93JP-0286985.

PR 28-DEC-1993; 93JP-0334773.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Kitada C, Odaka A, Suzuki N;

DR WPI; 1994-264110/32.

PT Antibodies recognising specific parts of beta-amyloid - can be
 used for diagnosis of diseases implicating beta-amyloid, such as
 Alzheimer's disease

PS Claim 7; Page 85; 116pp; Japanese.

CC Antibodies which recognise specific subfragments of the beta-amyloid
 CC protein are claimed. Specifically, the antibodies (which are pref.
 CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
 CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
 CC from the C-terminal portion. The antibodies are useful for assaying
 CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
 CC disease.

XX

```
SQ Sequence 16 AA;

Query Match 100.0%; Score 12; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-07; 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12
   |||||
Db 1 daefrhdsgyev 12

RESULT 5
AAW35344
ID AAW35344 standard; peptide; 16 AA.
XX
AC AAW35344;
XX
DT 17-APR-1998 (first entry)
XX
DE Human beta-amyloid precursor 16-mer peptide.
XX
KW Beta-amyloid precursor polypeptide; acetylcholinesterase; AChE;
KW neuronal degeneration; Parkinson's disease; Alzheimer's disease;
KW stroke; cancer; calcium channel modulator; antibody; inhibitor.
XX
OS Homo sapiens.
XX
PN WO9735962-A1.
XX
PD 02-OCT-1997.
XX
PF 21-MAR-1997; 97WO-GB00796.
XX
PR 22-MAR-1996; 96GB-0006040.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Greenfield SA, Vaux DJ;
XX
DR WPI; 1997-489626/45.
XX
KW Peptide(s) from acetylcholine esterase which open calcium channels -
PT used for treating disorders of the central nervous system, cancer
PT and stroke
XX
PS Claim 3; Page 20; 27pp; English.
XX
CC This 16-mer peptide is present in a region of the beta-amyloid precursor
CC polypeptide. This region lies at the amino acid terminus of the 42
CC residue peptide which accumulates in Alzheimer's disease. The 16-mer
CC has at least 70% homology with the beta-amyloid precursor. This peptide
CC is known to act alone or in synergism with a fragment of
CC acetylcholinesterase (AAW35340-W35343) to contribute to neuronal
CC degeneration. Compounds that inhibit the biological activity of the
CC novel peptides, and antibodies, can be used to control cytoplasmic
CC calcium ion currents in vivo, and are useful for treating disorders of
CC the central nervous system (e.g. Parkinson's and Alzheimer's diseases),
CC stroke and cancer.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 12; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-07; 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12
   |||||
Db 1 daefrhdsgyev 12

RESULT 6
AAW35344
ID AAW35344 standard; peptide; 16 AA.
XX
AC AAW35344;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human amyloid beta-A4 peptide fragment Cys-betaA4(1-16).
XX
KW Amyloid beta-A4 peptide; human; amyloid-specific aptamer; nootropic;
KW neuroprotective; antidiabetic; antiparkinsonian; anticonvulsant;
KW
```

```
AAV49693
ID AAV49693 standard; peptide; 16 AA.
XX
AC AAV49693;
XX
DT 13-JAN-2000 (first entry)
XX
DE Human beta amyloid precursor protein antigenic peptide #2.
XX
KW Human; beta amyloid precursor protein; APP; beta secretase inhibition;
KW alpha secretase; neurological disorder; Alzheimer's disease;
KW Down syndrome; mutation.
XX
OS Homo sapiens.
XX
PN WO9951752-A1.
XX
PD 14-OCT-1999.
XX
PF 31-MAR-1999; 99WO-JP01701.
XX
PR 31-MAR-1998; 98JP-0101821.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Ozawa K, Ikeda S, Tabira T;
XX
DR WPI; 1999-620208/53.
XX
KW A cell line which produces beta amyloid precursor protein, used in the
PT investigation of neurological disorders such as Alzheimer's disease -
XX
PS Disclosure: Page 42; 70pp; Japanese.
XX
CC The present invention describes a cell line which produces beta amyloid
CC precursor protein (APP) and expresses alpha secretase activity but
CC expresses beta secretase activity only under an external stimulus.
CC Also described is a cloning method for DNA encoding beta secretase,
CC comprising: (1) inserting a DNA library into the cell line, expressing
CC the inserted DNA, and selecting cells expressing beta secretase then
CC isolating the beta secretase DNA from them; or (2) isolating nucleic
CC acid from the cell line with or without external stimulation and
CC performing subtractive cloning to identify DNA expressed only under
CC stimulation. Products from the present invention may be used in the
CC investigation of neurological disorders such as Alzheimer's disease
CC and Down syndrome and in particular the association of mutations of
CC the beta APP with them. The present sequence represents a human
CC beta APP peptide.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 12; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-07; 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12
   |||||
Db 1 daefrhdsgyev 12

RESULT 7
AAB11496
ID AAB11496 standard; Protein; 17 AA.
XX
AC AAB11496;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human amyloid beta-A4 peptide fragment Cys-betaA4(1-16).
XX
KW Amyloid beta-A4 peptide; human; amyloid-specific aptamer; nootropic;
KW neuroprotective; antidiabetic; antiparkinsonian; anticonvulsant;
KW
```

KW diagnosis; treatment; Alzheimer's disease; spongiform encephalopathy;
 KW type II diabetes mellitus; Parkinson's disease; Huntington's chorea.
 OS Homo sapiens.
 PN DE19916417-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 01-APR-1999; 99DE-1016417.
 XX
 PR 01-APR-1999; 99DE-1016417.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Erdmann VA, Fuerste JP, Dahmen FY, Seilheimer B;
 XX WPI; 2000-657337/64.
 DR
 XX New amyloid-specific aptamer, useful for diagnosis and/or treatment of
 PT e.g. Alzheimer's disease, is stabilized against nucleases -
 XX
 PS Examples; Page 16; 62pp; German.
 CC This invention describes novel amyloid-specific aptamers (I) that are
 CC stabilized against nucleic acid-degrading enzymes, and its alleles and/or
 CC derivatives. The products of the invention have neurotropic,
 CC neuroprotective, antidiabetic, antiparkinsonian and anticonvulsant
 CC activity. (I), and their mixtures, are used for diagnosis (when labeled)
 CC and/or treatment of Alzheimer's disease, spongiform encephalopathies and
 CC type II diabetes mellitus, Parkinson's disease, spongiform encephalopathies and
 CC (I) have high affinity for amyloid (typically dissociation constant is in
 CC the micromolar range) and are simple to prepare. They are stabilized so
 CC that their half-life in the serum is over 1 minute, particularly over 1
 CC day. (I) are selected in vitro, contrast monoclonal antibodies that are
 CC selected in animals or cell lines and are subject to variation, and can
 CC be prepared very reproducibly by chemical synthesis, optionally with
 CC reporter molecules incorporated at exactly defined locations. They are
 CC also easier to denature reversibly.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 12; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEV 12
 DB 2 daefrhdsgyev 13
 |||||
 RESULT 8
 ABA48345
 ID ABA48345 standard; peptide; 17 AA.
 XX
 AC ABA48345;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Beta-amyloid antigenic peptide (Abetal-16).
 XX
 KW Beta-amyloid; neurotropic; neuroprotective; vaccine; antibody; brain;
 KW amyloid plaque; Alzheimer's disease; antigen.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 17
 FT /note= "C-terminal amide"
 XX
 PN W0200077178-A1.
 XX

PD 21-DEC-2000.
 XX
 PF 15-JUN-2000; 2000WO-US16551.
 XX
 PR 16-JUN-1999; 99US-0139408.
 XX
 PA (BOST-) BOSTON BIOMEDICAL RES INST.
 XX
 PI Raso V;
 XX
 DR WPI; 2001-112220/12.
 XX
 PT New antibodies which catalyze hydrolysis of beta-amyloid at a
 PT predetermined amide linkage, useful for e.g. sequestering or reducing
 PT free beta-amyloid in the bloodstream and brain and preventing formation
 PT of amyloid plaques -
 XX
 PS Example 1; Fig 2; 82pp; English.
 CC The invention relates to an antibody which catalyzes the hydrolysis of
 CC beta-amyloid at a predetermined amide linkage. The antibodies are useful
 CC for sequestering free beta-amyloid in the bloodstream of an animal,
 CC reducing beta-amyloid levels in the brain, preventing formation of
 CC amyloid plaques, and disaggregating amyloid plaques present in the brain,
 CC thus may be used in treating patients diagnosed with or at risk for
 CC Alzheimer's disease. The present sequence represents a beta-amyloid
 CC antigenic peptide made from the N-terminal sequence of beta-amyloid. The
 CC antigenic peptides were designed to be tested for suitability to
 CC antibody-mediated therapy.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 12; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEV 12
 DB 1 daefrhdsgyev 12
 |||||
 RESULT 9
 AAW08361
 ID AAW08361 standard; peptide; 21 AA.
 XX
 AC AAW08361;
 XX
 DT 05-SEP-1997 (first entry)
 XX
 DE Beta-secretase substrate #3.
 XX
 KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
 KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
 XX
 OS Synthetic.
 XX
 PN W09640885-A2.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09985.
 XX
 PR 07-JUN-1995; 95US-0485152.
 PR 07-JUN-1995; 95US-0480498.
 XX
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 XX
 PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
 PI Mcconlogue LC, Sinha S, Tan H;
 XX
 DR WPI; 1997-052304/05.
 XX

XX Sequences AAY33752-Y33756 are synthetic oligopeptides used for measuring
CC the activity of beta-secretase (AAY33741). Beta-secretase is capable of
CC cleaving beta-amyloid protein precursor (APP) (AAY33742). These

CC carboxy, alkoxycarbamoyl, ureido, amidino, guanidino, cyano, azido,
 CC mercapto, alkylthio, alkylsulphoxy, alkylsulphonyl, alkylsulphenyl,
 CC aminosulphonyl, fluoro, chloro, bromo, iodo, alkyl or perfluoroalkyl;
 CC R4 = H, or an optionally branched alkyl group. The preparation is used to
 CC purify the hyperforin and/or adhyperforin content in St. John's Wort
 CC extracts. The obtained salts are storage stable and can be used in
 CC pharmaceutical compositions for the treatment of Alzheimer's disease and
 CC its symptoms. This sequence represents a fragment of the human secretase
 CC SEC-beta2 protein which is used to illustrate the method of the
 XX invention.
 SQ Sequence 21 AA;

Query Match 100.0%; Score 12; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 Db 2 daefrhdsgyev 13
 |||||

RESULT 12

AAB47265
 ID AAB47265 standard; Peptide; 21 AA.
 XX
 AC AAB47265;

DT 18-JUL-2001 (first entry)

DE Peptide 5-16' SW, for used in beta-secretase assay.

KW Beta-secretase; isotype; beta-amyloid precursor protein; APP;
 KW beta-amyloid peptide; beta-AP; Alzheimer's disease; Downs syndrome;
 KW HCHWA-D; Swedish mutation; maltose binding protein; MBP.

XX Synthetic.

PN US6221645-B1.

XX 24-APR-2001.

PF 07-JUN-1996; 96US-0660531.

PR 07-JUN-1995; 95US-0480498.

PA (ELAN-) ELAN PHARM INC.

PI Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H, McConlogue LC;
 DR WPI; 2001-315578/33.

XX Novel antibody that specifically binds native beta-secretase protein,
 PT useful for raising anti-idiotypic antibodies and for detecting or
 PT diagnosing pathological conditions related to presence of respective
 PT antigens

PS Example; Column 30; 42pp; English.

CC The sequences given in AAB47262-67 represent synthetic peptides
 CC containing the cleavage sites derived from wild-type beta-amyloid
 CC precursor protein (APP). These peptides were used in assays utilising
 CC partially purified beta-secretase to identify beta-secretase inhibitors.
 CC Beta-secretase is thought to be responsible for the pathogenic
 CC processing of APP to form beta amyloid peptide (beta-AP) in beta-AP
 CC related conditions, e.g. Alzheimer's disease, Downs syndrome, HCHWA-D
 CC etc. Beta-secretase has a molecular weight of 260-300 kD and will bind
 CC to wheat germ agglutinin but not to concanavalin A. Beta-secretase
 CC will cleave both the wild type and the Swedish mutation of APP.

XX Sequence 21 AA;

Query Match 100.0%; Score 12; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 Db 6 daefrhdsgyev 17
 |||||

RESULT 13

AAR07753
 ID AAR07753 standard; protein; 22 AA.

XX
 AC AAR07753;

DT 22-FEB-1991 (first entry)

DE Bta-amyloid protirin, SCVAP2.

KW Monoclonal antibody SV17-6E10; Down's syndrome; Alzheimer's disease;
 KW beta-amyloid precursor; amyloid plaques.

XX Synthetic.

PN WO9012871-A.

XX 01-NOV-1990.

XX 13-APR-1990; 90WO-US02003.

XX 14-APR-1989; 89US-0338983.

PA (REME-) RES FOUND MENTAL HY.

PI Kim KS, Wisniewski HM, Wen GY, Chen CMJ, Sapienza VJ;

XX WPI; 1990-348474/46.

XX Cerebrovascular amyloid protein-specific monoclonal antibody
 PT SV17-6E10 - for immunoassay of peptide whose levels are raised in
 PT Down's syndrome or Alzheimer's disease patients

XX Example 4; page 11; 24pp; English.

CC This peptide is used in a "Double Ab Sandwich Immunoassay" to
 CC detect beta-amyloid protein. SV17-6E10 MAB(capture Ab) is used
 CC to coat microtitre plate wells. The plate is then washed (dist-
 CC lled water), coated with PBS(TGB) and this (SCVAP2) protein is
 CC added. The plate is washed and a 2nd Ab (detection Ab), MAb 4G8-
 CC This double Ab sandwich ELISA test is a highly sensitive and
 CC accurate detection system for the beta-amyloid protein.

CC See also AAR07752.

XX Sequence 22 AA;

Query Match 100.0%; Score 12; DB 11; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 Db 1 daefrhdsgyev 12
 |||||

RESULT 14

AAP90381
 ID AAP90381 standard; protein; 28 AA.

XX
 AC AAP90381;

DT 01-NOV-1989 (first entry)

XX Synthetic A4 amyloid peptide.
 DE
 XX
 XX Synthetic: A4 amyloid polypeptide; Alzheimer's disease;
 KW immunoassays; antibodies.
 XX
 XX Synthetic.
 OS
 XX WO8906242-A.
 PN
 XX 13-JUL-1989.
 PD
 XX 11-OCT-1988; 88WO-US03590.
 PF
 XX 08-OCT-1987; 87US-0105751.
 PR
 XX (MCLE) MCLEAN HOSPITAL CORP; (UYRO) UNIVERSITY OF ROCHESTER.
 PA
 XX Majocha R, Marotta CA, Zain S;
 PI WPI; 1989-220551/30.
 DR
 XX Antibodies to A4 amyloid polypeptide
 PT - used in immunoassays and for imaging of A4 amyloid
 PT in Alzheimer's diseased patients.
 PT
 XX Claim 1; page 27; 30pp; English.
 PS
 XX Synthetic A4 amyloid polypeptide (see also AAP90382, AAP90383).
 CC Used as immunogen, (un)coupled, or to produce antibodies. Used in
 CC immunoassays and for imaging of A4 amyloid in Alzheimer's disease.
 CC
 XX Sequence 28 AA;
 SQ

Query Match 100.0%; Score 12; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 |||||
 DB 1 daefrhdsgyev 12

RESULT 15
 AAR54702
 ID AAR54702 standard; peptide; 28 AA.
 XX
 XX AAR54702;
 AC
 XX 15-DEC-1994 (first entry)
 DT
 XX Beta-amyloid fragment (1-28).
 DE
 XX Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.
 KW
 XX Homo sapiens.
 OS
 XX WO9409364-A.
 PN
 XX 28-APR-1994.
 PD
 XX 13-OCT-1993; 93WO-US09772.
 PF
 XX 13-OCT-1992; 92US-0959251.
 PR
 XX (UYDU-) UNIV DUKE.
 PA
 XX Strittmatter WJ;
 PI
 XX WPI; 1994-151484/18.
 DR
 XX Immoobilised beta-amyloid protein or fragments - used in assays
 PT

PT for obtaining prods for use in the diagnosis and treatment of
 PT disorders such as Alzheimer's disease.
 XX
 XX Claim 4; Page 28; 49pp; English.
 PS
 XX A construct comprising a beta-amyloid protein (BAP) or fragment (esp.
 CC the peptides given in AAR54702-03) immobilised on a solid support can be
 CC used to detect cpds. which bind to BAP. Binding of proteins in
 CC human cerebrospinal fluid proteins were shown to bind to beta-
 CC amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28)
 CC was used as control.
 CC
 XX Sequence 28 AA;
 SQ

Query Match 100.0%; Score 12; DB 15; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 |||||
 DB 1 daefrhdsgyev 12

RESULT 16
 AAR60368
 ID AAR60368 standard; peptide; 28 AA.
 XX
 XX AAR60368;
 AC
 XX 15-MAR-1995 (first entry)
 DT
 XX Beta-amyloid (1-28).
 DE
 XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
 KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
 KW
 XX Homo sapiens.
 OS
 XX WO9417197-A.
 PN
 XX 04-AUG-1994.
 PD
 XX 24-JAN-1994; 94WO-JP00089.
 PF
 XX 25-JAN-1993; 93JP-0010132.
 PR
 XX 05-FEB-1993; 93JP-0019035.
 PR
 XX 16-NOV-1993; 93JP-0286985.
 PR
 XX 28-DEC-1993; 93JP-0334773.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Kitada C, Odaka A, Suzuki N;
 PI WPI; 1994-264110/32.
 DR
 XX Antibodies recognising specific parts of beta-amyloid - can be
 PT used for diagnosis of diseases implicating beta-amyloid, such as
 PT Alzheimer's disease
 PT
 XX Claim 7; Page 84; 116pp; Japanese.
 PS
 XX Antibodies which recognise specific subfragments of the beta-amyloid
 CC protein are claimed. Specifically, the antibodies (which are pref.
 CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
 CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
 CC from the C-terminal portion. The antibodies are useful for assaying
 CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
 CC disease.
 CC
 XX Sequence 28 AA;
 SQ

```
Query Match      100.0%; Score 12; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
   | | | | | | | | | |
Db 1 daefrhdsgyev 12

RESULT 17
AAR64170
ID AAR64170 standard; peptide; 28 AA.
XX
AC AAR64170;
XX
DT 03-AUG-1995 (first entry)
XX
DE A4-O(1-28) a partial beta amyloid peptide.
XX
KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
KW Down's syndrome; A4-O(1-28).
XX
OS Synthetic.
XX
PN WO9428412-A.
XX
PD 08-DEC-1994.
XX
PF 27-MAY-1994; 94WO-US05809.
XX
PR 28-MAY-1993; 93US-0069010.
XX
PA (MIRI-) MIRIAM HOSPITAL.
XX
PI Majocha RE, Marotta CA;
XX
DR WPI; 1995-023013/03.
XX
PT Amyloid binding composition comprising labelled amyloid protein
PT and carrier - useful for in vivo imaging of amyloid deposits, for
PT diagnosing Alzheimer's disease and Down's Syndrome.
XX
PS Example 1; Page 23; 58pp; English.
XX
CC AAR64170, the A4-O(1-28) polypeptide is the first 28 amino acids of the
CC 4.2 kD peptide deriv. from senile plaque cores of an AD (Alzheimer's
CC disease) brain, known as beta amyloid. A4-O has strong aggregation
CC properties, and binds to itself strongly. This peptide is used to obtain
CC and select beta amyloid proteins that can be used for in vivo imaging
CC of amyloid deposits and hence diagnosis of an amyloidosis-associated
CC disease, such as AD or Down's syndrome. AAR64165 shows the generic
CC sequence of the amyloid protein for generation of variants.
XX
SQ Sequence 28 AA;

Query Match      100.0%; Score 12; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
   | | | | | | | | | |
Db 1 daefrhdsgyev 12

RESULT 18
AAR64172
ID AAR64172 standard; peptide; 28 AA.
XX
AC AAR64172;
XX
DT 03-AUG-1995 (first entry)
XX
```

```
XX
DE A4-B(1-28) a partial beta amyloid peptide.
XX
KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
KW Down's syndrome; A4-B(1-28).
XX
OS Synthetic.
XX
PN WO9428412-A.
XX
PD 08-DEC-1994.
XX
PF 27-MAY-1994; 94WO-US05809.
XX
PR 28-MAY-1993; 93US-0069010.
XX
PA (MIRI-) MIRIAM HOSPITAL.
XX
PI Majocha RE, Marotta CA;
XX
DR WPI; 1995-023013/03.
XX
PT Amyloid binding composition comprising labelled amyloid protein
PT and carrier - useful for in vivo imaging of amyloid deposits, for
PT diagnosing Alzheimer's disease and Down's Syndrome.
XX
PS Example 3; Page 23; 58pp; English.
XX
CC AAR64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of
CC the AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of
CC the 28 amino acids are different from the A4-O(1-28) peptide shown in
CC AAR64170. A4-O has strong aggregation properties, and binds to itself
CC strongly. It is used to obtain and select beta amyloid proteins that can
CC be used for in vivo imaging of amyloid deposits and hence diagnosis of
CC an amyloidosis-associated disease, such as AD or Down's syndrome.
CC AAR64165 shows the generic sequence of the amyloid protein for generation
CC of variants.
XX
SQ Sequence 28 AA;

Query Match      100.0%; Score 12; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
   | | | | | | | | | |
Db 1 daefrhdsgyev 12

RESULT 19
AAR64173
ID AAR64173 standard; Protein; 28 AA.
XX
AC AAR64173;
XX
DT 20-JAN-1997 (first entry)
XX
DE Beta/A4-amyloid peptide residues 1-28.
XX
KW Beta/A4-amyloid peptide; tissue plasminogen activator;
KW Alzheimer's disease; stimulation; investigation; pathogenesis;
KW hereditary cerebral haemorrhage with amyloidosis-butch type;
KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
XX
OS Homo sapiens.
XX
PN WO9615799-A1.
XX
PD 30-MAY-1996.
XX
```

PF 22-NOV-1995; 95WO-US15007.

XX 22-NOV-1994; 94US-0347144.

XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX Anderson S;

XX WPI; 1996-268332/27.

XX Use of agents which bind beta-amyloid peptide - for diagnosis,
PT prevention and treatment of vascular damage caused by amyloid
PT deposits, partic. in haemorrhaging and Alzheimer's disease

XX Example 1; Fig 1; 52pp; English.

XX To investigate the effects of beta-amyloid peptide (BAP) on
CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
CC One peptide contained 42 amino acids and corresp. to the full
CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained
CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
CC (HCHWA-D), respectively. In an assay to determine the effect of
CC the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)
CC gave 1st order rate constant of activation (k(app)) values of
CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null
CC and fibrinogen controls. The results demonstrate that the BAP are
CC able to stimulate t-PA activity in vitro, which is significant in
CC that it provides a means for investigating and controlling the
CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
CC angiopathy related cerebral haemorrhage.

XX Sequence 28 AA;

Query Match 100.0%; Score 12; DB 17; Length 28;

Best Local Similarity 100.0%; Pred. No. 6.7e-07;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

Db 1 daefrhdsgyev 12

RESULT 20

AAW01414

ID AAW01414 standard; Protein; 28 AA.

XX AAW01414;

XX 20-JAN-1997 (first entry)

XX Beta/A4-amyloid peptide residues 1-28 Dutch.

XX Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;
XX Alzheimer's disease; stimulation; investigation; pathogenesis;
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;
KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
KW hemorrhage.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 22

XX /note= "wild type Glu substd. with Gln"

XX W09615799-A1.

XX 30-MAY-1996.

XX 22-NOV-1995; 95WO-US15007.

XX 22-NOV-1994; 94US-0347144.

XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX Anderson S;

XX WPI; 1996-268332/27.

XX Use of agents which bind beta-amyloid peptide - for diagnosis,
PT prevention and treatment of vascular damage caused by amyloid
PT deposits, partic. in haemorrhaging and Alzheimer's disease

XX Example 1; Fig 1; 52pp; English.

XX To investigate the effects of beta-amyloid peptide (BAP) on
CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
CC One peptide contained 42 amino acids and corresp. to the full
CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained
CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
CC (HCHWA-D), respectively. In an assay to determine the effect of
CC the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)
CC gave 1st order rate constant of activation (k(app)) values of
CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null
CC and fibrinogen controls. The results demonstrate that the BAP are
CC able to stimulate t-PA activity in vitro, which is significant in
CC that it provides a means for investigating and controlling the
CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
CC angiopathy related cerebral haemorrhage.

XX Sequence 28 AA;

Query Match 100.0%; Score 12; DB 17; Length 28;

Best Local Similarity 100.0%; Pred. No. 6.7e-07; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12

Db 1 daefrhdsgyev 12

RESULT 21

AAV39805

ID AAV39805 standard; peptide; 28 AA.

XX AAV39805;

XX 29-NOV-1999 (first entry)

XX Beta-amyloid protein, Beta/A4 amyloid (1-28).

XX Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
KW long-standing inflammation; malignancy; Familial Mediterranean Fever;
KW multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
KW carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
KW endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
KW Creutzfeldt-Jakob disease; Gerstmann Strausler Syndrome;
KW subacute spongiform encephalopathy; therapy.

XX Homo sapiens.

XX US958883-A.

XX 28-SEP-1999.

XX 05-JUN-1995; 95US-0461216.

XX 23-OCT-1992; 92US-0969734.

XX 23-SEP-1992; 92US-0950417.

XX (UNIW) UNIV WASHINGTON.

XX SHOW AD;

XX WPI; 1999-561062/47.
 XX Peptides of 6-8 amino acids useful for treating or preventing
 PT amyloidosis -
 PS
 XX Disclosure: Column 67-68; 83pp; English.
 CC This sequence represents a fragment of the beta-amyloid protein. The
 CC invention relates to a method for treating or preventing a form of
 CC amyloidosis, including Alzheimer's disease using this sequence. The
 CC compositions may be useful for treating or preventing the amyloidosis
 CC associated with long-standing inflammation, various forms of malignancy
 CC (including B-cell type malignancies), Familial Mediterranean Fever,
 CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
 CC Creutzfeldt-Jakob disease, Gerstmann Strausler Syndrome, kuru, scrapie
 CC and other subacute spongiform encephalopathies.
 XX Sequence 28 AA;

Query Match 100.0%; Score 12; DB 20; Length 28;
 Best Local Similarity 100.0%; Pred. NO. 6.7e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
 Db 1 daefrhdsgyev 12
 |||||

RESULT 22
 AAY39806
 ID AAY39806 standard; peptide; 28 AA.
 AC AAY39806;

DT 29-NOV-1999 (first entry)

XX Beta-amyloid protein fragment.

XX Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
 KW long-standing inflammation; malignancy; Familial Mediterranean Fever;
 KW multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
 KW carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
 KW endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
 KW Creutzfeldt-Jakob disease; Gerstmann Strausler Syndrome;
 KW subacute spongiform encephalopathy; therapy.

XX Homo sapiens.

OS US958883-A.

PN 28-SEP-1999.

XX 05-JUN-1995; 95US-0461216.

PR 23-OCT-1992; 92US-0969734.

XX 23-SEP-1992; 92US-0950417.

PA (UNIW) UNIV WASHINGTON.

XX Snow AD;

DR WPI; 1999-561062/47.

XX Peptides of 6-8 amino acids useful for treating or preventing
 PT amyloidosis -

PS Disclosure: Column 69-70; 83pp; English.

CC This sequence represents a fragment of the beta-amyloid protein. The
 CC invention relates to a method for treating or preventing a form of
 CC amyloidosis, including Alzheimer's disease using this sequence. The
 CC compositions may be useful for treating or preventing the amyloidosis
 CC associated with long-standing inflammation, various forms of malignancy
 CC (including B-cell type malignancies), Familial Mediterranean Fever,
 CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
 CC Creutzfeldt-Jakob disease, Gerstmann Strausler Syndrome, kuru, scrapie
 CC and other subacute spongiform encephalopathies.
 XX Sequence 28 AA;

Qy 1 DAEFRHDSGYEV 12
 Db 1 daefrhdsgyev 12
 |||||

Query Match 100.0%; Score 12; DB 20; Length 28;
 Best Local Similarity 100.0%; Pred. NO. 6.7e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 23
 AAW81467

ID AAW81467 standard; peptide; 28 AA.

AC AAW81467;

DT 28-JAN-1999 (first entry)

XX Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).

XX Amyloid beta; Abeta; deoxygenerated solvent; evaporative deposition;
 KW research; neurotoxicity; free-radical; glutamine synthetase.

OS Synthetic.

XX US5840838-A.

PN 24-NOV-1998.

XX 29-FEB-1996; 96US-0609090.

PR 29-FEB-1996; 96US-0609090.

XX (KENT) UNIV KENTUCKY RES FOUND.

XX Aksekov M, Butterfield DA, Carney JM, Hensley K;
 PI WPI; 1999-034120/03.

XX Process for treating synthetic amyloid beta peptides - by organic
 PT solvent treatment, useful for studying neurotoxicity

XX Claim 5; Columns 9-10; 14pp; English.

XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenerated
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
 CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
 CC 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta
 CC peptides are useful as research tools for studying neurotoxicity
 CC resulting from Abeta peptide -enhanced free-radical production. The
 CC treatment increases the activity of the synthetic Abeta peptides in tests
 CC to determine free-radical generating capacity and glutamine synthetase
 CC inactivation.


```
Db 1 daefrhdsgeyev 12
|||||
RESULT 26
AAB91816
ID AAB91816 standard; Peptide; 28 AA.
XX AC
XX AAB91816;
XX DT
XX 22-JUN-2001 (first entry)
XX DE
XX Amyloid beta-protein fragment peptide SEQ ID NO:992.
XX KW
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX KW blood component; modification; succinimidyl; maleimido group; amino;
XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX OS
XX Homo sapiens.
XX OS Synthetic.
XX PN
XX WO200069900-A2.
XX PD
XX 23-NOV-2000.
XX PF
XX 17-MAY-2000; 2000WO-US13576.
XX PR
XX 17-MAY-1999; 99US-0134406.
XX PR
XX 10-SEP-1999; 99US-0153406.
XX PR
XX 15-OCT-1999; 99US-0159783.
XX PA
XX (CONJ-) CONJUCHEM INC.
XX PI
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX PT peptidase degradation, useful for increasing length of in vivo activity
XX PT
XX
XX Disclosure; Page 519; 733pp; English.
XX
The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 28 AA;
XX
Query Match 100.0%; Score 12; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGEYEV 12
|||||
Db 1 daefrhdsgeyev 12
|||||
RESULT 27
AAB49396
ID AAB49396 standard; peptide; 28 AA.
XX AC
XX AAB49396;
XX DT
XX 06-MAR-2001 (first entry)
XX DE
XX Human amyloid peptide protein fragment SEQ ID NO: 11.
XX KW
XX Human; immunogenic peptide; immune response; monophosphoryl lipid A;
XX KW antigen; infection; cancer; amyloid deposition.
XX OS
XX Homo sapiens.
XX PN
XX WO200069456-A2.
XX PD
XX 23-NOV-2000.
XX PF
XX 12-MAY-2000; 2000WO-US13156.
XX PR
XX 13-MAY-1999; 99US-0133963.
XX PA
XX (AMCY ) AMERICAN CYANAMID CO.
XX PI
XX Hagen M;
XX WPI; 2001-024946/03.
XX DR
XX
XX Antigenic composition having an antigen (e.g. viral protein) and an
XX PT adjuvant, useful for enhancing humoral and cellular immune response in
XX PT a host or as a prophylaxis against virus, bacterium, parasite, cancer
XX PT cell or allergen .
XX PS
XX Disclosure; Page 40; 129pp; English.
XX
The present invention provides an antigenic composition comprising an
CC antigen with a 3'-O-deacylated monophosphoryl lipid A or monophosphoryl
CC lipid A adjuvant. The presence of the adjuvant causes an increased immune
CC response. The antigen may be from a pathogenic bacterium, fungus, virus
CC or parasite, a cancer cell, an allergen or from amyloid peptide protein.
CC The composition can be used in the prevention and treatment of infection,
CC cancer and diseases caused by amyloid deposition. It is particularly
CC useful against HIV, Neisseria gonorrhoeae and respiratory syncytial
CC virus.
XX
XX Sequence 28 AA;
XX
Query Match 100.0%; Score 12; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGEYEV 12
|||||
Db 1 daefrhdsgeyev 12
|||||
RESULT 28
AAB35590
ID AAB35590 standard; peptide; 28 AA.
XX AC
XX AAB35590;
XX DT
XX 15-FEB-2001 (first entry)
XX DE
XX Human clone B(1-28) amyloid B peptide.
XX KW
XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
XX KW acute cardiovascular disease; therapy.
XX OS
XX Homo sapiens.
XX
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Fri Sep 13 09:18:10 2002

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PN US6136548-A.
XX
PD 24-OCT-2000.
XX
PF 02-SEP-1999; 99US-0388890.
XX
PR 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Anderson S;
XX
DR WPI; 2001-030939/04.
XX
PT Identifying mutant tissue-type plasminogen activator (t-PA) for
PT improving thrombolytic therapy or treating vascular hemorrhaging, by
PT determining whether t-PA binds to fibrin but not to a beta amyloid
PT peptide -
XX
PS Example 3; Column 26; 23pp; English.
XX
CC The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 12; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 daefrhdsgyev 12

RESULT 30
AAB35598
ID AAB35598 standard; peptide; 28 AA.
XX
AC AAB35598;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human clone H14Q B(1-28) amyloid B peptide.
XX
KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW acute cardiovascular disease; therapy.
XX
OS Homo sapiens.
XX
PN US6136548-A.
XX
PD 24-OCT-2000.
XX
PF 02-SEP-1999; 99US-0388890.
XX
PR 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Anderson S;
XX
DR WPI; 2001-030939/04.
XX
PT Identifying mutant tissue-type plasminogen activator (t-PA) for
PT improving thrombolytic therapy or treating vascular hemorrhaging, by
PT determining whether t-PA binds to fibrin but not to a beta amyloid
PT peptide -
XX
PS Example 3; Column 26; 23pp; English.
XX
CC The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 12; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 daefrhdsgyev 12

RESULT 29
AAB35597
ID AAB35597 standard; peptide; 28 AA.
XX
AC AAB35597;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human clone H13Q B(1-28) amyloid B peptide.
XX
KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW acute cardiovascular disease; therapy.
XX
OS Homo sapiens.
XX
PN US6136548-A.
XX
PD 24-OCT-2000.
XX
PF 02-SEP-1999; 99US-0388890.
XX
PR 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Anderson S;
XX
DR WPI; 2001-030939/04.
XX
```

ID	Sequence	28 AA;
XX	AAB35600 standard; peptide; 28 AA.	
XX	AAB35600;	
XX	15-FEB-2001 (first entry)	
XX	Human clone E22Q B(1-28) amyloid B peptide.	
XX	Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;	
XX	acute cardiovascular disease; therapy.	
XX	Homo sapiens.	
XX	US6136548-A.	
XX	24-OCT-2000.	
XX	02-SEP-1999; 99US-0388890.	
XX	26-JUL-1996; 96US-0686959.	
XX	22-NOV-1994; 94US-0347144.	
XX	22-NOV-1995; 95WO-US15007.	
XX	(RUTF) UNIV RUTGERS STATE NEW JERSEY.	
XX	Anderson S;	
XX	WPI; 2001-030939/04.	
XX	Identifying mutant tissue-type plasminogen activator (t-PA) for improving thrombolytic therapy or treating vascular hemorrhaging, by determining whether t-PA binds to fibrin but not to a beta amyloid peptide -	
XX	Example 3; Column 26; 23pp; English.	
XX	The present invention describes a method for identifying mutant derivatives of tissue-type plasminogen activator, which involves determining whether or not they bind to beta-amyloid peptides and fibrin. Mutants will only bind to the latter. These mutants are useful in improved thrombolytic therapies, in the treatment of Alzheimer's disease and in the treatment of acute cardiovascular disease, which may be caused by myocardial infarction, stroke, ischaemia and pulmonary embolism.	
XX	Sequence 28 AA;	
XX	Query Match 100.0%; Score 12; DB 22; Length 28;	
XX	Best Local Similarity 100.0%; Pred. No. 6.7e-07;	
XX	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	Qy 1 DAEFRHDSGYEV 12	
XX	Db 1 daefrhdsgyev 12	
XX	RESULT 33	
XX	AAB36201	
XX	ID AAB36201 standard; peptide; 28 AA.	
XX	AAB36201;	
XX	15-FEB-2001 (first entry)	
XX	Human clone D23Q B(1-28) amyloid B peptide.	
XX	Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;	
XX	acute cardiovascular disease; therapy.	
XX	Homo sapiens.	
XX	US6136548-A.	
XX	US6136548-A.	
XX	24-OCT-2000.	
XX	02-SEP-1999; 99US-0388890.	
XX	26-JUL-1996; 96US-0686959.	
XX	22-NOV-1994; 94US-0347144.	
XX	22-NOV-1995; 95WO-US15007.	
XX	(RUTF) UNIV RUTGERS STATE NEW JERSEY.	
XX	Anderson S;	
XX	WPI; 2001-030939/04.	
XX	Identifying mutant tissue-type plasminogen activator (t-PA) for improving thrombolytic therapy or treating vascular hemorrhaging, by determining whether t-PA binds to fibrin but not to a beta amyloid peptide -	
XX	Example 3; Column 26; 23pp; English.	
XX	The present invention describes a method for identifying mutant derivatives of tissue-type plasminogen activator, which involves determining whether or not they bind to beta-amyloid peptides and fibrin. Mutants will only bind to the latter. These mutants are useful in improved thrombolytic therapies, in the treatment of Alzheimer's disease and in the treatment of acute cardiovascular disease, which may be caused by myocardial infarction, stroke, ischaemia and pulmonary embolism.	
XX	Sequence 28 AA;	
XX	Query Match 100.0%; Score 12; DB 22; Length 28;	
XX	Best Local Similarity 100.0%; Pred. No. 6.7e-07;	
XX	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	Qy 1 DAEFRHDSGYEV 12	
XX	Db 1 daefrhdsgyev 12	
XX	RESULT 32	
XX	AAB35600	

PD 24-OCT-2000.
XX
PF 02-SEP-1999; 99US-0388890.
XX
PR 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
XX
PI Anderson S;
XX
XX WPI; 2001-030939/04.
XX
XX Identifying mutant tissue-type plasminogen activator (t-PA) for
PT improving thrombolytic therapy or treating vascular hemorrhaging, by
PT determining whether t-PA binds to fibrin but not to a beta amyloid
PT peptide -
XX
XX Example 3; Column 26; 23pp; English.
XX
XX The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
XX Sequence 28 AA;
SQ
Query Match 100.0%; Score 12; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
Db 1 daefrhdsgyev 12
RESULT 34
AAW81468
ID AAW81468 standard; peptide; 28 AA.
XX
XX AAW81468;
XX
XX 28-JAN-1999 (first entry)
XX
XX Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30).
DE
XX Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
KW
XX Synthetic.
XX
XX US5840838-A.
XX
XX 24-NOV-1998.
XX
XX 29-FEB-1996; 96US-0609090.
XX
XX 29-FEB-1996; 96US-0609090.
XX
XX (KENT) UNIV KENTUCKY RES FOUND.
PA
XX Aksenov M, Butterfield DA, Carney JM, Hensley K;
PI WPI; 1999-034120/03.
XX
XX Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
PT
XX Claim 5; Columns 9-10; 14pp; English.
XX
XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/mL, incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC "evaporative deposition" in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide -enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.

PD 24-OCT-2000.
XX
PF 02-SEP-1999; 99US-0388890.
XX
PR 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
XX
PI Anderson S;
XX
XX WPI; 2001-030939/04.
XX
XX Identifying mutant tissue-type plasminogen activator (t-PA) for
PT improving thrombolytic therapy or treating vascular hemorrhaging, by
PT determining whether t-PA binds to fibrin but not to a beta amyloid
PT peptide -
XX
XX Example 3; Column 26; 23pp; English.
XX
XX The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
XX Sequence 28 AA;
SQ
Query Match 100.0%; Score 12; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
Db 1 daefrhdsgyev 12
RESULT 34
AAB36202
ID AAB36202 standard; peptide; 28 AA.
XX
XX AAB36202;
XX
XX 15-FEB-2001 (first entry)
XX
XX Human clone K280 B(1-28) amyloid B peptide.
DE
XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW acute cardiovascular disease; therapy.
KW
XX Homo sapiens.
OS
XX US6136548-A.
PN
XX 24-OCT-2000.
PD
XX 02-SEP-1999; 99US-0388890.
XX
XX 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
PA
XX Anderson S;
PI WPI; 2001-030939/04.
XX
XX Identifying mutant tissue-type plasminogen activator (t-PA) for

```

XX SQ Sequence 30 AA;
Query Match 100.0%; Score 12; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 daefrhdsgyev 12
|||||

RESULT 36
AAW08359
ID AAW08359 standard; peptide; 33 AA.
AC AAW08359;
XX
DT 05-SEP-1997 (first entry)
DE Beta-secretase substrate #1.
XX
KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
XX
OS Synthetic.
XX
PN W09640885-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96W0-US09985.
XX
PR 07-JUN-1995; 95US-0485152.
XX
PR 07-JUN-1995; 95US-0480498.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
PI Mcconlogue LC, Sinha S, Tan H;
XX
WPI; 1997-052304/05.
XX
Beta-secretase which specifically cleaves beta-amyloid precursor
protein - useful to screen for inhibitors useful in treatment of
Alzheimer's disease
XX
Disclosure; Page 44; 92pp; English.
XX
AAW08359-W08362 represent substrates for the enzyme of the invention.
XX
The enzyme of the invention is beta-secretase, and specifically cleaves
beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP
is thought to occur via cleavage between residues 16 and 17 of the
beta-amyloid peptide region by an alpha-secretase. Pathogenic processing
is thought to occur by beta-secretase cleavage of beta-APP.
XX
Beta-secretase activity can be detected and measured using a method of
the invention, which detects at least one of the beta-secretase cleavage
products formed on cleavage. The method can be used to determine whether
a test substance inhibits proteolytic cleavage, by beta-secretase, of
beta-APP. Compounds effective to at least partially inhibit
beta-secretase activity can be used to inhibit cleavage of beta-APP in
cells or mammalian hosts. Isolation and purification of beta-secretase
will permit chemical modelling of a critical event in the pathology of
Alzheimer's disease.
XX
SQ Sequence 33 AA;
Query Match 100.0%; Score 12; DB 18; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 30 AA;
Query Match 100.0%; Score 12; DB 20; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 1 daefrhdsgyev 29
|||||

RESULT 37
RAY33753
ID AAY33753 standard; Protein; 33 AA.
AC AAY33753;
XX
DT 09-NOV-1999 (first entry)
DE Synthetic oligopeptide 17-16'SW.
XX
KW Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
KW Alzheimer's disease; measure activity; cleavage site.
XX
OS Synthetic.
XX
PN US5942400-A.
XX
PD 24-AUG-1999.
XX
PF 07-JUN-1996; 96US-0659984.
XX
PR 07-JUN-1996; 96US-0659984.
XX
PR 07-JUN-1995; 95US-0480498.
XX
PR 07-JUN-1995; 95US-0485152.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Anderson JP, Jacobson-Croak KL, Sinha S;
XX
WPI; 1999-517417/43.
XX
A method for detecting human beta-secretase cleavage of polypeptides
useful for identifying beta-secretase inhibitors
XX
Examples; Column 30; 43pp; English.
XX
Sequences AAY33752-Y33756 are synthetic oligopeptides used for measuring
the activity of beta-secretase (AAY33741). Beta-secretase is capable of
cleaving beta-amyloid protein precursor (APP) (AAY33742). These
synthetic peptides contain the cleavage site of APP. Beta-secretase and
APP are used in a method for detecting human beta-secretase cleavage of
polypeptides and for identifying beta-secretase inhibitors. Inhibition
of beta-secretase activity would be useful for chemical modelling of a
critical event in the pathology of Alzheimer's disease. Inhibitors of
beta-secretase would be useful for the prevention and treatment of
Alzheimer's disease and Down's Syndrome.
XX
SQ Sequence 33 AA;
Query Match 100.0%; Score 12; DB 20; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 18 daefrhdsgyev 29
|||||

RESULT 38
AAW98002
ID AAW98002 standard; Protein; 33 AA.
XX
AC AAW98002;
XX
DT 21-JUN-1999 (first entry)
XX
DE Amyloid precursor protein (aa656-678) with Swedish mutation.
```

```
XX Amyloid precursor protein; APP; human; gene targeting;
KW homologous recombination; transgenic mouse; transgenic animal;
KW animal model; Alzheimer's disease.
XX
OS Mus musculus.
XX WO9909150-A1.
XX 25-FEB-1999.
XX
XX 18-AUG-1997; 97WO-US14507.
XX 18-AUG-1997; 97WO-US14507.
XX (FARB ) BAYER CORP.
XX
XX Wirak DO;
XX
XX WPI: 1999-181029/15.
XX
XX Modification of target nucleic acids - by homologous recombination,
PT used particularly for introducing a humanised amyloid precursor
PT protein gene into rodents for producing models of Alzheimer's
PT disease
XX
XX Disclosure; Page 145; 209pp; English.
XX
XX This polypeptide comprises residues 656-678 of a murine amyloid
CC precursor protein (APP). The invention provides a novel gene
CC targeting strategy that facilitates the introduction of one or
CC more specific mutations into any gene in a single double reciprocal
CC homologous recombination step. The method has been used
CC particularly for introducing a humanised APP gene into rodents for
CC producing animal models of Alzheimer's disease (AD). 4 independent
CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
CC have been created using the gene targeting technique applied to
CC embryonic stem cells. In each line, the mouse APP gene was modified
CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues
CC 666-770 of APP770 were encoded by human cDNA sequences instead of
CC mouse genomic exons (exons 16-18). Within these residues, only 3
CC amino acid differences exist between the mouse and human proteins,
CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
CC exon-cDNA fusion gene therefore encodes an APP containing a
CC humanised beta-amyloid domain. Swedish- and/or London-FAD APP
CC mutations have also been introduced (see also AAW97997-W98001).
XX
XX Sequence 33 AA;
XX
XX Query Match 100.0%; Score 12; DB 20; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-07;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DAEFRHDSGYEV 12
XX Db 1 daefrhdsgyev 12
XX
XX RESULT 39
XX AAW81469
XX ID AAW81469 standard; peptide; 33 AA.
XX
XX AC AAW81469;
XX
XX 28-JAN-1999 (first entry)
XX
XX Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).
XX
XX Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
XX Synthetic.
XX
```

```
XX US5840838-A.
XX
XX 24-NOV-1998.
XX
XX 29-FEB-1996; 96US-0609090.
XX
XX 29-FEB-1996; 96US-0609090.
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Aksenov M, Butterfield DA, Carney JM, Hensley K;
XX WPI: 1999-034120/03.
XX
XX Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
PT
XX
XX Claim 5; Columns 9-10; 14pp; English.
XX
XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide -enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.
XX
XX Sequence 33 AA;
XX
XX Query Match 100.0%; Score 12; DB 20; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-07;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DAEFRHDSGYEV 12
XX Db 1 daefrhdsgyev 12
XX
XX RESULT 40
XX AAB47263
XX ID AAB47263 standard; Peptide; 33 AA.
XX
XX AC AAB47263;
XX
XX 18-JUL-2001 (first entry)
XX
XX Peptide 17-16'SW, for used in beta-secretase assay.
XX
XX Beta-secretase; isotype; beta-amyloid precursor protein; APP;
XX beta-amyloid peptide; beta-AP; Alzheimer's disease; Downs syndrome;
KW HCHWA-D; Swedish mutation; maltose binding protein; MBP.
XX
XX Synthetic.
XX
XX US6221645-B1.
XX
XX 24-APR-2001.
XX
XX 07-JUN-1996; 96US-0660531.
XX
XX 07-JUN-1995; 95US-0480498.
XX (ELAN-) ELAN PHARM INC.
XX
XX Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H, McConlogue LC;
PI
```


XX WPI; 2001-315578/33.
 XX Novel antibody that specifically binds native beta-secretase protein,
 PT useful for raising anti-idiotypic antibodies and for detecting or
 PT diagnosing pathological conditions related to presence of respective
 PT antigens -
 XX Example: Column 29; 42pp; English.
 PS The sequences given in AAB47262-67 represent synthetic peptides
 CC containing the cleavage sites derived from wild-type beta-amyloid
 CC precursor protein (APP). These peptides were used in assays utilising
 CC partially purified beta-secretase to identify beta-secretase inhibitors.
 CC Beta-secretase is thought to be responsible for the pathogenic
 CC processing of APP to form beta amyloid peptide (beta-AP) in beta-AP
 CC related conditions, e.g. Alzheimer's disease, Downs syndrome, HCHWA-D
 CC etc. Beta-secretase has a molecular weight of 260-300 kD and will bind
 CC to wheat germ agglutinin but not to concanavalin A. Beta-secretase
 CC will cleave both the wild type and the Swedish mutation of APP.
 XX Sequence 33 AA;
 SQ
 Query Match 100.0%; Score 12; DB 22; Length 33;
 Best Local Similarity 100.0%; Pred. No. 7.8e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDSGYEV 12
 Db | | | | | | | | | |
 18 daefrhdsgyev 29
 RESULT 41
 ID AAW02335 standard; peptide; 35 AA.
 XX AAW02335;
 AC
 DT 06-MAY-1997 (first entry)
 XX Beta-amyloid peptide residues 1-20, 26-40.
 DE
 XX Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX Synthetic.
 OS
 XX WO9628471-A1.
 PN
 XX 19-SEP-1996.
 PD
 XX 14-MAR-1996; 96WO-US03492.
 PF
 XX 27-OCT-1995; 95US-0548998.
 PR
 XX 14-MAR-1995; 95US-0404831.
 PR
 XX 07-JUN-1995; 95US-0475579.
 XX (PHAR-) PHARM PEPTIDES INC.
 PA Benjamin H, Chin J, Findeis MA, Garnick MB, Geffer ML;
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
 PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
 XX WPI; 1996-433762/43.
 DR
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (indirectly) to at least 1 modifying gp., useful in

PT treatment of Alzheimer's disease
 XX Claim 29; Page 82; 106pp; English.
 PS AAW02333-W02336 represent beta-amyloid peptide fragments that can be
 CC used in the modulator compounds of the invention. Beta-amyloid peptide
 CC is a 4 kilodalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients.
 CC The amyloid modulators of the invention comprise an amyloidogenic protein
 CC or peptide (see AAW02310-W02336) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as decaim, a cholanyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease.
 XX Sequence 35 AA;
 SQ
 Query Match 100.0%; Score 12; DB 17; Length 35;
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDSGYEV 12
 Db | | | | | | | | | |
 1 daefrhdsgyev 12
 RESULT 42
 ID AAW47228 standard; peptide; 35 AA.
 XX AAW47228;
 AC
 XX 22-MAY-1998 (first entry)
 DT
 DE Beta-amyloid peptide residues 1-35.
 XX Screening assay; beta-amyloid peptide; treatment;
 KW amyloidosis disease; Alzheimer's disease.
 XX Homo sapiens.
 OS
 XX US5721106-A.
 PN
 XX 24-FEB-1998.
 PD
 XX 12-SEP-1994; 94US-0304585.
 PF
 XX 12-SEP-1994; 94US-0304585.
 PR
 XX 13-AUG-1991; 91US-0744767.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA (MINU) UNIV MINNESOTA.
 PI Maggio JE, Mantyh PW;
 XX WPI; 1998-168404/15.
 DR
 XX New in vitro screening assay for Alzheimer's disease drugs -
 PT comprises assessing binding of labelled beta-amyloid peptide to silk
 PT sample

XX Claim 8; Columns 31-32; 36pp; English.

PS The present sequence was used in the development of a novel in

XX vitro screening assay for agents capable of affecting the

CC deposition of beta-amyloid peptide (BAP) on tissue. The method

CC comprises contacting a silk sample with labelled BAP, optionally

CC in the presence of a test agent, detecting the amount of label

CC bound to the silk and assessing the effect of the agent on the

CC deposition of BAP. Agents that inhibit binding of BAP to silk are

CC potentially useful for treating amyloidosis diseases, especially

CC Alzheimer's disease.

XX Sequence 35 AA:

SQ

Query Match 100.0%; Score 12; DB 19; Length 35;

Best Local Similarity 100.0%; Pred. No. 8.2e-07; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12

Db 1 daefrhdsgyev 12

|||||

RESULT 43

AAW89355

ID AAW89355 standard; peptide; 35 AA.

XX

AC AAW89355;

XX

DT 02-MAR-1999 (first entry)

XX

DE Beta-amyloid peptide derivative A-beta-1-20,26-40.

XX

KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;

KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;

KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;

KW Creutzfeldt-Jakob disease; BAP.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US5854204-A.

XX

XX 29-DEC-1998.

XX

XX 14-MAR-1996; 96US-0612785.

XX

XX 14-MAR-1996; 96US-0612785.

PR 14-MAR-1995; 95US-0404831.

PR 07-JUN-1995; 95US-0475579.

PR 27-OCT-1995; 95US-0548998.

XX

XX (PRAE-) PRAECIS PHARM INC.

XX

XX Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;

PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;

PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;

XX

XX WPI; 1999-094964/08.

DR

XX New peptide(s) derived from beta-amyloid peptide that inhibit

PT amyloid aggregation - and neurotoxicity, specifically for treatment

PT and prevention of Alzheimer's disease

XX

XX Claim 3; Column 71-72; 52pp; English.

PS

XX The present invention describes beta-amyloid peptide (BAP) derivatives.

XX The BAP derivatives inhibit aggregation of amyloidogenic proteins and

CC peptides, specifically BAP, and their neurotoxicity, so are useful for

CC treating and preventing any disease involving amyloidosis, specifically

CC Alzheimer's disease but also Down's syndrome, familial amyloid

CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and

CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose

CC these diseases, in vitro or in vivo, by detecting binding of BAP to

CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation

CC even when BAP is present in molar excess. The present sequence

CC represents a BAP derivative.

XX

SQ Sequence 35 AA;

Query Match 100.0%; Score 12; DB 20; Length 35;

Best Local Similarity 100.0%; Pred. No. 8.2e-07; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEV 12

Db 1 daefrhdsgyev 12

|||||

RESULT 44

AAW89359

ID AAW89359 standard; peptide; 35 AA.

XX

AC AAW89359;

XX

DT 02-MAR-1999 (first entry)

XX

DE Beta-amyloid peptide derivative A-beta-1-25,31-40 (Delta26-30).

XX

KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;

KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;

KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;

KW Creutzfeldt-Jakob disease; BAP.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US5854204-A.

XX

XX 29-DEC-1998.

XX

XX 14-MAR-1996; 96US-0612785.

XX

XX 14-MAR-1996; 96US-0612785.

PR 14-MAR-1995; 95US-0404831.

PR 07-JUN-1995; 95US-0475579.

PR 27-OCT-1995; 95US-0548998.

XX

XX (PRAE-) PRAECIS PHARM INC.

XX

XX Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;

PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;

PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;

XX

XX WPI; 1999-094964/08.

DR

XX New peptide(s) derived from beta-amyloid peptide that inhibit

PT amyloid aggregation - and neurotoxicity, specifically for treatment

PT and prevention of Alzheimer's disease

XX

XX Claim 7; Column 81-82; 52pp; English.

PS

XX The present invention describes beta-amyloid peptide (BAP) derivatives.

XX The BAP derivatives inhibit aggregation of amyloidogenic proteins and

CC peptides, specifically BAP, and their neurotoxicity, so are useful for

CC treating and preventing any disease involving amyloidosis, specifically

CC Alzheimer's disease but also Down's syndrome, familial amyloid

CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and

CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose

CC these diseases, in vitro or in vivo, by detecting binding of BAP to

CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation

CC even when BAP is present in molar excess. The present sequence

CC represents a BAP derivative.

```

XX SQ Sequence 35 AA;
Query Match 100.0%; Score 12; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 1 daefrhdsgyev 12
|||||
|

RESULT 45
AAW89360
ID AAW89360 standard; peptide; 35 AA.
XX
AC AAW89360;
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-1-15,21-40 (Delta16-20).
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; BAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
(PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findels WA, Garnick MB, Geffer ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Mollineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
WPI; 1999-094964/08.
XX
DR New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
PS Claim 8; Column 81-82; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bap) derivatives.
CC The bap derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bap, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bap derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bap to
CC labelled bap derivatives. Some bap derivatives inhibit bap aggregation
CC even when bap is present in molar excess. The present sequence
CC represents a bap derivative.
XX
SQ Sequence 35 AA;
Query Match 100.0%; Score 12; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 1 daefrhdsgyev 12
|||||
|

RESULT 46
AAW81471
ID AAW81471 standard; peptide; 36 AA.
XX
AC AAW81471;
XX
DT 28-JAN-1999 (first entry)
XX
DE Synthetic amyloid beta (Abeta) peptide 6 (residues 1-36).
XX
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
OS Synthetic.
XX
PN US5840838-A.
XX
PD 24-NOV-1998.
XX
PF 29-FEB-1996; 96US-0609090.
XX
PR 29-FEB-1996; 96US-0609090.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
XX
WPI; 1999-034120/03.
XX
DR Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
PT
XX
PS Claim 5; Columns 11-12; 14pp; English.
XX
CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC //evaporative deposition// in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide-enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.
XX
SQ Sequence 36 AA;
Query Match 100.0%; Score 12; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 1 daefrhdsgyev 12
|||||
|

RESULT 47
AAW60362
ID AAW60362 standard; peptide; 38 AA.
XX
AC AAW60362;
XX

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DT 15-MAR-1995 (first entry)
XX Beta-amyloid (1-38).
DE
XX
XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis.
XX
XX Homo sapiens.
OS
XX W09411797-A.
PN
XX
XX 04-AUG-1994.
PD
XX
XX 24-JAN-1994; 94WO-JP00089.
PF
XX
XX 25-JAN-1993; 93JP-0010132.
PR
XX 05-FEB-1993; 93JP-0019035.
PR
XX 16-NOV-1993; 93JP-0286985.
PR
XX 28-DEC-1993; 93JP-0334773.
PR
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX Kitada C, Odaka A, Suzuki N;
XX
XX WPI; 1994-264110/32.
DR
XX
XX Antibodies recognising specific parts of beta-amyloid - can be
PT used for diagnosis of diseases implicating beta-amyloid, such as
PT Alzheimer's disease
PT
XX
XX Disclosure; Page 81; 116pp; Japanese.
PS
XX
XX Antibodies which recognise specific subfragments of the beta-amyloid
CC protein are claimed. Specifically, the antibodies (which are pref.
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
CC from the C-terminal portion. The antibodies are useful for assaying
CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
CC disease.
XX
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 12; DB 15; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
DB 1 daefrhdsgyev 12
RESULT 48
AAW92722
ID AAW92722 standard; peptide; 38 AA.
XX
XX AAW92722;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #68.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
XX Homo sapiens.
OS
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
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XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX
XX Yankner BA;
PI
XX
XX WPI; 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PT
XX
XX Claim 1b; Column 39-40; 28pp; English.
PS
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 12; DB 20; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEV 12
DB 1 daefrhdsgyev 12
RESULT 49
AAB91799
ID AAB91799 standard; Peptide; 38 AA.
XX
XX AAB91799;
AC
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Amyloid beta-protein fragment peptide SEQ ID NO:975.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX W0200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR
XX 10-SEP-1999; 99US-0153406.
PR
XX 15-OCT-1999; 99US-0159783.
PR
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX
XX WPI; 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
```

XX PS Disclosure; Page 513; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

XX SQ Sequence 38 AA;

Query Match 100.0%; Score 12; DB 22; Length 38;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

Db |||||

1 daefrhdsgyev 12

RESULT 50

AAB91826

ID AAB91826 standard; Peptide; 38 AA.

AC AAB91826;

XX 22-JUN-2001 (first entry)

DT Anyloid beta-protein fragment peptide SEQ ID NO:1002.

DE Protection; endogenous therapeutic peptide; peptidase; conjugation;

XX blood component; modification; succinimidyl; maleimido group; amino;

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

PN 23-NOV-2000.

PD 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

DR Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

PT

XX Disclosure; Page 522; 733pp; English.

PS The present invention describes a modified therapeutic peptide (I)

CC

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

XX SQ Sequence 38 AA;

Query Match 100.0%; Score 12; DB 22; Length 38;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

Db |||||

1 daefrhdsgyev 12

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Job time: 135 sec

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